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July 28, 2004, 08:49:47; Search time 37.7711 Seconds (without alignments) 793.576 Million cell updates/sec
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490
1 LHFVDQYREQLIARVTSVEV........HLIMELWEKGSKKGLLPLSS 95
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                       OM protein - protein search, using sw model
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1: Sp_acteria:*

2: Sp_bacteria:*

3: Sp_fungi:*

5: Sp_maman:*

6: Sp_mamman:*

7: Sp_mamman:*

7: Sp_mamman:*

8: Sp_page:*

9: Sp_page:*

1: Sp_rodent:*

1: Sp_rodent:*

2: Sp_virus:*

1: Sp_virus:*

2: Sp_virus:*

3: Sp_virus:*

3: Sp_virus:*

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6: Sp_virus:*

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
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                                                                                                                                                                                                                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q8hxk9 bos taurus	Q8chk8 rattus norv	Q8xnw6 clostridium	Q8en79 oceanobacil	Q8gbv1 pseudomonas	Q8g977 pseudomonas	Q9z5v9 pseudomonas	O52212 pseudomonas	Q9x7j2 pseudomonas	Q8zsg2 pyrobaculum	Q966f3 caenorhabdi	Q8k4e9 mus musculu	Q921f0 mus musculu	Q95q18 caenorhabdi	Q8ykj7 anabaena sp	Q84f19 pantoea agg
	ID	<u>овнхкэ</u>	QBCHK8	QBXNW6	QBEN79	Q8GBV1	Q8G977	Q9Z5V9	052212	Q9X7J2	Q8ZSQ2	Q966F3	Q8K4E9	Q921F0	Q95Q18	Q8YKJ7	Q84FL9
	08	9	11	16	16	7	7	7	N	7	17	ហ	11	11	S	16	7
	Query Match Length DB	195	193	Н	614		260	338	404	425	193	254	376	376	295	482	734
۴۰	Query Match	48.6	42.9	17.2	16.8	16.2	16.2	16.2	16.2	16.2	15.9	15.9	15.8	15.8	15.5	15.3	15.2
	Score	238	210	84.5	82.5	79.5	79.5	79.5	79.5	79.5	78	78	77.5	77.5	94	75	74.5
	Result No.	1	2	m	4	Ŋ	9	7	œ	σ	10	11	12	13	14	15	16

Q9plz8 campylobact			Q8epp9 oceanobacil			Q86nf3 caenorhabdi	Q80xa9 mus musculu	O59062 pyrococcus		mus		Q8jzn0 mus musculu	Q81tv0 bacillus an	Q98ps5 mycoplasma	Q99q59 strongyloce	Q81s17 vitis vinif	Q801r9 xenopus lae		070522 rattus norv	O17460 schistosoma							Q41236 solanum tub	Q9iwb1 soil-borne
	11 Q8K4E7			11 Q8K4E8	11 Q8K4E6	5 Q86NF3	11 Q80XA9					н		G					н		12 Q91NQ3						10 Q41236	
584	376	630	175	376	376	267	630	197	251	252	315	376	592	691	870	96	453	609	379	406	788	870	871	610	771	265	368	1816
15.0	14.9	14.8	14.7	14.7	14.7	14.6	14.6	14.5	14.3		14.3		14.3	14.3	14.3	14.2	14.2	14.2	14.1	14.1	14.1	14.1				٠	13.9	٠
73.5	73	72.5	72	72	72	71.5	71.5	71	70	7.0	70	70	70	70	70	69.5	69.5	69.5	69	69	69	69	69	68.5	68.5	68	68	68
17	18	19	20	21	22	23	24	25	26	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8EN79;
Q8EN79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
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Q8EN79
           g
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Masumoto J., Zhou W., Chen F.F., Su F., Kuwada J.Y., Hidaka E.,

Masumoto J., Zhou W., Chen F.F., Su F., Kuwada J.Y., Hidaka E.,

Katsuyama T., Sagara J., Taniguchi S., Ngo-Hazelett P.,

Postlethwait J.H., Nunnez G., Inohara N.;

"Caspy: A Zebrafish caspase activated by ASC oligomerization required

"To pharyngeal Arch development.";

J. Boll. Chem. 0:0-0/2022.

REMBL, AB053165; BAC43754.1;

ROJ. GO:00056325; Cintracellular; IEA.

GO; GO:0006329; F:apoptosis; IEA.

ROJ. GO:0006915; P:apoptosis; IEA.

RINTERPO: IPR001315; CARD.

RINTERPO: IPR001315; CARD.

R PROSITE; PS50209; CARD.

R PROSITE; PS50209; CARD.

R PROSITE; PS50209; CARD.
                                                                                                                                                                                                                                                                                                                                                                                        1 LHFVDQYREQLIARVTSVEVVLDKLHGQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 HFVDQYREQLIARVISVEVVLDKIHGQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDRK 61
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                             Length 195;
                                                                                                                                                                                                                                             48.6%; Score 238; DB 6; Length 19
58.0%; Pred. No. 7.7e-17;
ive 15; Mismatches 19; Indels
GO, GO:0016329; F:apoptosis regulator activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
InterPro; IPR0040315; CARD.
InterPro; IPR0040315; CARD.
Pfam; PF02758; PAAD DAPIN, 1.
PROSTIE; PS560249; CARD; 1.
PROSTIE; PS560249; DAPIN, 1.
SEQUENCE 195 AA; 21917 MW; 7C9D4BDBA9A9E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21654 MW; F3B27B560D86A17B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Apoptosis-associated speck-like protein.
RASC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 TCKDLLLQALRDTQPYLVDDL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KCKDGLYQALKETHPHLIMEL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | : : | : | : : | 1.1 | | 1.2 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 CKDGLYQALKETHPHLIMEL 81
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 58.0%
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            112
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(TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)

PRT; 1175 AA.

PRELIMINARY;

DBXNW6

OBXNW6 ID O8 AC O8 DT 01 DT 01

RESULT 3

Q8XNW6; 01-MAR-2002 (01-MAR-2002 (

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RECUENCE FROM N.A.

RECUENCE FROM N.A.

RECUENCE FROM N.A.

REQUENCE FROM N.A.

RECUENCE TEXALN=12253076;

RECUENCE TEXALN=122520767;

RECUENCE STRAIN=122520767;

RECUENCE SECUENCE OF Cocanobacillus ineyensis isolated from the Ineya Takami H., Takaki Y., Uchiyama I.;

Recuence Sequence of Cocanobacillus ineyensis isolated from the Ineya RT Ridge and its unexpected adaptive capabilities to extreme environments.";

RECUENCE Acids Res. 30:3927-3935(2002).

RELIA PROVIDED RECUENCE SOURCE STRAIN—10000 STRAIN STRA
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EMBL; ARO03185; BAB79922.1; -. GO; GO:0016020; Cmembrane; IEA.
GO; GO:0016020; Cmembrane; IEA.
GO; GO:004009; P:ATP-binding; IEA.
GO; GO:004009; P:ATP-binding cassette (ABC) transporter acti. .; IEA.
GO; GO:004009; P:ATP-binding cassette (ABC) transporter acti. .; IEA.
GO; GO:00439; PECCENTIONER CASSETTE ACTION COMPLETE COMPLETE ACTION COMPLETE AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 VDQYREQLIARVTSVEVVLDKLHGQVLSQEQYERVLAE-NTRPSQMR-----KLFSLS 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                  Clostridium perfringens.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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NCBL_TaxID=182710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Asparagine synthetase (EC 6.3.5.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.2%; Score 84.5; DB 16; 26.1%; Pred. No. 5.7; tive 26; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            984 ESIKKKLEEQRDILHIKAKQEHKLALLSDLEK 1015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     614 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=13 / Type A;
MEDLINE=21664373; PubMed=11792842;
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les 24; Conservative
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Probable exonuclease.
SBCC OR CPE0216.
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MEDLINE=22313464; PubMed=12426347;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hill K.E., Weightman A.J.;
"Horizontal transfer of dehalogenase genes on IncP-beta plasmids
"Horizontal transfer of dehalogenase genes on IncP-beta plasmids
during bacterial adaptation to degrade alpha-halocarboxylic acids.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AJS-84809, CADS-9131.1;
GO; GO:0003877; F:DNA binding; IEA.
GO; GO:0004803; F:transposase activity; IEA.
GO; GO:0004803; F:transposase activity; IEA.
FIREPRO, IPR002560; Transposase_12.
Pfam; PF01610; Transposase_12; 1.
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Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
                                                                                                                                                                                                                                  464 MSQLLDRKDRMSMGASLEVRVPFADHRLVEYVWNIPWDIKWVNGHEKGIL 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                          Length 614;
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01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative transposase (Fragment).
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative transposase (Fragment).
                       16.8%; Score 82.5; DB 16; 26.4%; Pred. No. 4.3; ive 20; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.2%; Score 79.5; DB
32.1%; Pred. No. 3.3;
tive 9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=217730;
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                                                                     Conservative
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                                               Local Similarity
nes 29; Conserv
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Best Local
                          Query Match
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Q8GBV1
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120 YRAAVKAVLPQARIVVDKFHVVRWANDALERVRKGLRKELKPSQSRTL----KGDRXI- 173
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Appl. Environ. Microbiol. 65:2151-2162(1999).
EMBL; AF121970; AAD20008.1; -.
GO; GO:0003677; F:DAM binding: IEA.
GO; GO:0004803; F:Transposase activity; IEA.
GO; GO:000410; P:DNA recombination; IEA.
InterPro; IPRO2560; Transposase_12.
Ffam; PPO1610; Transposase_12.
Ffam; PRO1610; Transposase_12.
SEQUENCE 338 AA; 39711 MW; EOG3DF2EABE3B329 CRC64;
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BIDILINE=99240444; PubMed=10224014;
Tsoi T.v., Plotnikova E.G., Cole J.R., Guerin W.F., Bagdasarian M.,
Tiedje J.N.;
Weightman A.J., Topping A.W., Hill K.E., Lee L.;
"Investigation of two evolutionarily unrelated halocarboxylic acid dehalogenase gene families.";
J. Bacteriol. 184:6581-6591(2002).
EMBL, AJ534881; CAD59132.1;
EMBL, AJ534881; CAD59132.1;
CO, GO:0003677; F:DNA binding; IEA.
GO, GO:0004803; F:transposase activity; IEA.
GO, GO:0006310; P:DNA recombination; IEA.
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Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                         Length 260;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                           29;
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                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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1 Similarity 32.1%; Pred. No. 3.3;
27; Conservative 9; Mismatches
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NON TER 26
NON TER 260 SE0
SEQUENCE 260 AA; 30910 MW; 32
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01-MAY-1999 (TrEMBLrel. 10,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 32.1 es 27; Conservative
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Best Local Similarity
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SEQUENCE FROM N.A.
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Gaps

19;

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7 YREQLIARVISVEVVLDKLHGQVLSQEQYERV---LAENTRPSQMRKLFSLSQSWDRKCK 63
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MEDLINE=195440403; PubMed=10223973;
MEDLINE=1959404003; PubMed=10223973;
MACIVATION and inactivation of Pseudomonas stutzeri methylbenzene catabolism pathways mediated by a transposable element.";
Appl. Environ. Microbiol. 65:1876-1882(1999).
BMBL; AJ013352; CAB42636.1; -...
GO; GO:0003407; F:DNA binding; IEA.
GO; GO:0004803; F:transposase activity; IEA.
GO; GO:0006310; P:DNA recombination; IEA.
InterPro; IPR002560; Transposase_12.
Pfam; PF04610; Transposase 12; 1.
SEQUENCE 425 AA; 49494 WW; 4EE338A74655B6BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
                                                     16.2%; Score 79.5; DB 2; Length 404; 32.1%; Pred. No. 5.5; ive 9; Mismatches 29; Indels 19
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Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
   2B130E43026E5404 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-NDR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein PAR3635.
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Local Similarity 32.1%; Pred. No. 5.8;
les 27; Conservative 9; Mismatches
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STRAIN-IM2 / ATCC 51768 / DSM 7523;
MEDLINE-21664397; PubMed=11792869;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonadaceae; Pseudomonas.
   47498 MW;
                                                     Query Match
Best Local Similarity 32.1
Matches 27; Conservative
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   404 AA;
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      SEQUENCE
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SPECIESSS, marcescens; PLASMID=R471a;
MEDLINE=99.374835; PubMed=8366028;
HO C., Kulaeva O.I., Levine A.S., Woodgate R.;
"A rapid method for cloning mutagenic DNA repair genes: isolation of unun-complementing genes from multidrug resistance plasmids R391,
R446b, and R471a.";
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SEQUENCE FROM N.A.

SEQUENCES—SPLUTIGA; STRAIN=PP3; FLASMID=pWW0;

A WEDLINE=22313464; PubMed=12426347;

A WEDLINE=22313464; PubMed=12426347;

A WEDLINE=22313464; PubMed=12426347;

A WEDLINE=22313464; PubMed=124263634;

A Slater J.H. Thomas A.W.;

I Transposition of DEH, a Broad-Host-Range Transposon Flanked by I SPPUL2.

I SPPUL2.

I SPPUL2.

I SPPUL2.

I SPUL2.

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I STRAIN-RESIS STR
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MEDLINE=22313463; PubMed=12426346;
Williams P.A., Jones R.M., Shaw L.E.;
Milliams P.A., Jones R.M., Shaw L.E.;
A Third Transposable Element, ISPpul2, from the Toluene-Xylene catabolic Plasmid pWW0 of Pseudomonas putida mt-2.";
J. Bacteriol. 184:6572-6580(2002).
                                                                                                                                                                                                                                                                                           Plasmid pWW0, and Plasmid R471a.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=P.putida, PLASMID=pWW0;
Greated A., Lambertson L., Williams P.A., Thomas C.M.;
"Complete nucleotide sequence of IncP-9 plasmid pWW0.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                        Created)
Last sequence update)
Last annotation update)
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                                  404 AA.
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SPECIES-S.marcescens; PLASMID=R471a;
MEDLINE-98202731;
                               PRT;
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                                                                                        (TrEMBLrel. 06, (TrEMBLrel. 06, (TrEMBLrel. 25,
                                                                                                                                                                                Putative transposase (TnpA)
                                  PRELIMINARY;
                                                                                                                                                                                                                                            Pseudomonas putida, and
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Query Match
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Rhabditidae, Peloderinae, Caenorhabditis
                                                Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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STRAIN=DATE.

Waterston R.;

Tubirect Submission.";

E Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; ACC00689; AAK84575.1;

R GO; GO:0005743; C:mitochondrial inner membrane; IEA.

R GO; GO:000548; F:binding; IEA.

BR GO; GO:0006810; P:transport; IEA.

BR GO; GO:000810; P:transport; IEA.

BR InterPro; IPR001993; Mitoch carrier.

DR ROSITE; PS00215; MITOCH CARRIER; 1.
                                                                                                                                                                                                  Query Match 15.9%; Score 78; DB 17; Length 193; Best Local Similarity 27.4%; Pred. No. 3.3; Matches 23; Conservative 21; Mismatches 22; Indels
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to the EMBL/GenBank/DDBJ databases.
                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
EMBL; AE009943; AAL65061.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 193 AA; 21824 WW; 2456ADDEFB35DBA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q966F3;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein T13G4.6.
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STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
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"The sequence of C. e
Submitted (MAR-1999)
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155 INILKKPNQQPYANLISGRTPLGK-EGKLLTCFMGLRKYFLNCRPTKLKRLIRLVTHWVQ 213
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
similar to 2'-5' oligoadenylate synthetase 1B (2'-5'-oligoadenylate synthetase 1).
OASIA OR OASI.
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SEQUENCE FROM N.A.

SEQUENCE STAIN=MOLD/Rk;

X MEDINE=22103633; PubMed=12080145;

X Perelygin A.A., Scherbik S.V., Zhulin I.B., Stockman B.M., Li Y.,

A Brincon M.A.;

"Positional cloning of the murine flavivirus resistance gene.";

T Prositional cloning of the murine flavivirus resistance gene.";

PREMEL, AF418006; AAM47546.1; -.

RGD, MGI:97430; Oaslb.

R InterPro; IPR006117; 25A_SYNTH 2.

InterPro; IPR006116; 25A_SYNTH 2.

InterPro; IPR001201; PAP_25A_core.

R InterPro; IPR01201; PAP_25A_core.

R PROSITE; PS00833; 25A_SYNTH 3; 1.

R PROSITE; PS01823; 25A_SYNTH 3; 1.

R SEQUENCE 376 AA; 43919 MW; CFA34CABC3874842 CRC64;
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Nus musculus musculus (eastern Buropean house mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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SPECTES M. m.musculus, STRAIN=MBT/Pas;
MEDLINE=22177211; PubMed=12186974;
Mashimo T., Lucas M., Simon-Chazottes D., Frenkiel M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
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T-2002 (TrEMBLrel. 25, Last sequence update)
T-2003 (TrEMBLrel. 25, Last annotation update)
oligoadenylate synthetase 1B.
83 GLFQCXDG---QLRFVHPSFNSAQLLASHRRGFLP 115
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                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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01-OCT-2002
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Rhabditidae; Peloderinae; Caenorhabditis.
Montagutelli X., Ceccaldi P.E., Deubel V., Guenet J.L., Despres P., A. nonsenses mutation in the gene encoding 2'-5'-oligoadenylate synthetase/Ll isoform is associated with West Nile virus susceptibility in laboratory mice."; Proc. Netl. Acad. Sci. U.S.A. 99:11311-11316(2002).

EMBL; BC012877; AAN12877.1; -...

EMBL; AF466823; AAM97604.1; -...
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WOYMPEP; Y53F4B.39; CE24418.
InterPro; IPR001279; Blactmase-like.
Emi; PF00753; Lactamase B; 1.
SEQUENCE 295 AA; 33102 MW; 5D798FCSC67B97CB CRC64;
                                                                                                                                                                                                                                                                                          30F970452408FB7E CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KCKDGLYQALKETHPHLIMEL-----WEKGSK 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 AA
                                                                                                                 MGD; MGI:2180866; Oasia.

GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016740; F:RATP binding; IEA.
GO; GO:0016740; F:RATA binding; IEA.
GO; GO:0016740; F:RATA binding; IEA.
GO; GO:0016955; P:immune response; IEA.
InterPro; IPR006117; 25A_SYNTH_2.
InterPro; IPR006116; PAP_25A_core.
PROSITE; PS00833; 25A_SYNTH_2; I.REPOSITE; PS50152; 25A_SYNTH_2; I.REPOSITE; PS50152; 25A_SYNTH_3; I.SEQUENCE 376 AA; 43934 MW; 30F97045240B
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q95Q18 PRELIMINARY;
Q95Q18;
Q1-DEC-2001 (TYEMBLE1, 19, C1
Q1-DEC-2001 (TYEMBLE1, 19, Lk
Q1-JUN-2003 (TYEMBLE1, 24, Lk
Y53F4B.39 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               investigating biology.";
Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
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Best Local Similarity
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Q95Q18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Gaps
                                                                                                                                                                                                                                                                           Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Matanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
BMB1, AP053500, BAB57822.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16; Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
15.3%; Score 75; DB 16; Length 482
Best Local Similarity 24.1%; Pred. No. 20;
Matches 21; Conservative 21; Mismatches 35; Indels
                                                                                                                                                         Plasmid pc71120a1pha.
Bacteria; Cc7120a1pha.
Nostocales; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0046821, C:extrachromosonal DNA; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0015426; F:type I protein secretor activity; IEA.
GO; GO:0009306; P:type I protein secretion; IEA.
InterPro; IPR003997; RtxD.
PRINTS; PR01490; RTXTOXIND.
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 482 AA; 54120 MW; 95E4C016AAFCF66A CRC64;
                                                                   (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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Job time : 39.7711 secs
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=21595285; Pubmed=11759840;
                                                                                                                                                       Anabaena sp. (strain PCC 7120).
                                                                                                                    Hypothetical protein Alr7298.
                                   PRELIMINARY;
                                                                                                       (TrEMBLrel.
                                                                                                       01-JUN-2003
                                                                                                                                        ALR7298
                                 Q8YKJ7
RESULT 15
Q8YKJ7
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 28, 2004, 08:46:37; Search time 9.15663 Seconds

(without alignments)

540.228 Million cell updates/sec

Title:

US-09-996-617-2_COPY_1335_1429

Perfect score:

1 LHFVDQYREQLIARVTSVEV......HLIMELWEKGSKKGLLPLSS 95

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

___ Gapop 10.0 , Gapext 0.5
Searched: 141681 segs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Π				ASC_BRARE	CAR8 HUMAN	OAS1_PIG	LIN1 NYCCO	CAR4_HUMAN	CAR4_MOUSE	OAS3 HUMAN	SYL STRPN	OASE MOUSE	ENP2_CHICK	OAS1_HUMAN	SYL STRR6	BGAL_BACME	VNSC_PI1HB	VNSC_PI1HE	FLIG_BORBU	VIP CHICK	SYE_THETH	ZPRI CAEEL	SYL STAAM	SYL_STAAW	SYL_STRP8	YOUR BACSU	ACDL_PIG	MYSC_CHICK	OASI_RAT	C5P2_MOUSE	PHK2_RHIME		ACDL_HUMAN
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P11928 mus musculu P81177 staphylococ	Q8ds85 streptococc	Q61645 mus musculu	P32534 human parai	P58801 mus musculu	Q90660 gallus gall	P27986 homo sapien	O34098 spiroplasma	O83269 treponema p	Q9pib3 campylobact	P39057 anthocidari
OASA MOUSE	SYL STRMU	HAIR_MOUSE	VNSC PITHD	RIK2 MOUSE	BIR CHICK	P85A HUMAN	SPOT_SPICI	RPOB_TREPA	SYS CAMJE	DYHC_ANTCR
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64	6 4	64	63.5	63.5	63.5	63.5	63.5	63.5	63	63
£	3 0	37	38	33	4	41	42	43	44	45

ALIGNMENTS

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Apoptosis, ATP-binding, Leucine-rich repeat; Repeat,
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ASC_MOUSE
        SO THE BELL HERE BELL HER BELL HER BELL HERE BELL HER BELL HER BELL HER BELL HER BELL HER BELL HERE BELL HER BELL 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event-Alternative spliting; Named isoforms-4;
Name=1; Synonyms=NAC beta, DEFCAP-L;
Isold=200000-1; Sequence=Displayed;
Name=2; Synonyms=NAC alpha, DEFCAP-S;
Isold=202000-2; Sequence=VSP_004327;
Name=3; Synonyms=NAC gamma;
Isold=09C000-3; Sequence=VSP_004326, VSP_004327;
Name=4; Synonyms=NAC gamma;
Isold=09C0000-4; Sequence=VSP_004326,
Isold=09C0000-4; Sequence=VSP_004326,
-1- TISOUS PEECIFICITY: Widely expressed. Isoforms 1 and 2 are expressed in peripheral blood leukocytes, chronic myelogenous leukemia cell line K-562, followed by thymus, spleen and heart. Also detected in lung, placenta, small intestine, colon, kidney, liver and miscle
                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Interacts strongly with caspase 2, weakly with caspase 9 and with APAF1 in a cytochrome c-inducible way leading to the formation of an apoptosome. This interaction may be ATP-dependent. SUBCELLULAR LOCATION: Cytoplasmic.
ALTERNATIVE PRODUCTS:
                                                                                                                                                     Kochrer K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S., Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Able to form cytoplasmic structures termed death effector filaments. Enhances APAF1 and cytochrome c-dependent activation of pro-caspase-9 and consecutive apoptosis. Seems to bind ATP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      liver and muscle.

SIMILARITY: Contains 1 DAPIN domain.
SIMILARITY: Contains 1 NACHT domain.
SIMILARITY: Contains 1 CARD domain.
SIMILARITY: Contains 7 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MINI, 606652; C:intracellular; IC.

GO; GO:0005622; C:intracellular; IC.

GO; GO:0005625; F:caspase activator activity; NAS.

GO; GO:0006565; F:caspase activator activity; NAS.

GO; GO:0006919; F:caspase activation; NAS.

GO; GO:0006919; F:caspase activation; NAS.

GO; GO:0006917; P:induction of apoptosis; NAS.

InterPro; IPR001315; CARD.

InterPro; IPR001315; IRR RNinh.

InterPro; IPR001611; IRR RNinh.

INTERPRO; IPR00172; PAD_DAPIN, 1.

Pfam; PF05569; NACHT; 1.

PROSITE; PS50824; DAPIN; 1.

PROSITE; PS50824; DAPIN; 1.
                                                                                                                     SEQUENCE OF 282-1473 FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AF298548; AAG15254.1; --
EMBL, AF210105, AAG30288.1; --
EMBL, AF229069; AAK00748.1; --
EMBL, AF229060; AAK00749.1; --
EMBL, AF229060; AAK0079.1; --
EMBL, AF229062; AAK00751.1; --
EMBL, AB021143; BAA76770.1; --
EMBL, AB03143; BAA76770.1; --
FMRL, T17255; T17255.
for large proteins in vitro.";
DNA Res. 6:63-70(1999).
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1379 IHPVDQYREQLIARVTSVEVVLDKLHCQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDR 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LHFVDQYREQLIARVTSVEVVLDKLHGQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDR 60
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STRAIN=BALB/c; TISSUE=Thymus;
MEDLINE=20580347; PubMed=11139337;
MEDLINE=20580347; PubMed=11139337;
MEDLINE=20580347; Nakayama K., Ayukawa K., Sagara J.;
"Murine ortholog of ASC, a CARD-containing protein, self-associates and exhibits restricted distribution in developing mouse embryos.";
                                                                                                                                                                                                                                                                                                                                          Missing (in isolo....
/FTId=VSP 004326.
Missing (In isoform 2 and isoform 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASC MOUSE STANDARD; PRT; 193 AA.
Q9EPB4, Q9D2W9;
16-OCT-2001 (Rel. 40, Created)
10-OCT-2003 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Apoptosis-associated speck-like protein containing a CARD (mASC) (PYCARD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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[2]
SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Breast tumor;
Martinon F., Hofmann K., Tschopp J.;
Pycard a PYD and CARD containing molecule.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
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K->L: NO EFFECT.
K->S: NO EFFECT.
                                                                                                                                                                                                                                                                                                                           ATP (POTENTIAL)
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                                                            NACHT.
LRR 1.
LRR 2.
LRR 3.
LRR 4.
LRR 5.
LRR 6.
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Best Local Similarity
Matches 95; Conserv
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SEQUENCE FROM N.A.
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EMBL; BC008252; AAH08252.1; -.

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REAL SEQUENCE FROM N.A.

RAY SEQUENCE FROM N.A.

RAY STGUENCE C.F., Feling G.B., Wagner L., Shenmen C.M., Schuler G.D.,

RAY Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RAY STGUENCH N., Soares M.B., Bonaldow N.F., Rubin G.M., Hong L.,

RAY BOARK S.M., McEwan P.J., McKernan Y.D., Rasavant T.L., Scheetz T.E.,

RAY BOARK S.M., McEwan P.J., McKernan N.J., Malek J.A., Guntarathe P.H.,

RAY RICHARDS S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulpk S.W.,

RAY RICHARDS S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Guntarathe P.H.,

RAY RICHARDS S., Worley K.C., Hale S., Garcia A.M., Gay L.J., S., Sunchez A.D., Shelley S.W.,

RAY RICHARDS S., Morney D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RAY RICHARDS S., Morney D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RAY RICHARDS S., Morney D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RAY RICHARDS S., Schwill S., Schwulz S., Sanchez A.,

RAY Redriguez A.C., Grimwood J., Schwulz J., Wyers R.M.,

RAY Rodriguez A.C., Grimwood J., Schwulz J., Marra M.A.,

RAY Rodriguez A.C., Grimwood J., Schwulz J., Marra M.A.,

RAY ROLL Acad Scil J. Schwulz J., Warra M.A.,

RAY Recripted T.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,

RAY Recription and inlitial analysis of more than 15,000 full-length

RAY "Generation and inlitial analysis of more than 15,000 full-length

RAY "Generation and inlitial analysis of more than 15,000 full-length

C. -- SUBCELLULAR LOCATION: Cytoplasmic. Upstream of caspase activation,

C. -- SUBCELLULAR LOCATION: Cytoplasmic. Upstream of caspase activation,

REAL Acad Scil J. S.A. 991 Season Scillar Scillar Spherical ball-inker

C. -- SUBCELLULAR LOCATION: Cytoplasmic. Upstream of caspase activation,

C. -- SUBCELLULAR LOCATION: Cytoplasmic. Upstream of caspase activation,

REAL Scillar Specificative Scillar M.S. Scillar Scilla
RC STRAIN-C57BL/6J; TISSUE-Pancreas, and Tongue;
A Kawai J. Shinata K., Yoshino M., Itch M., Ishii Y.,
A Kawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
A rakawa T., Hara A., Shibata K., Komo H., Adachi J., Fukuda S.,
A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito T.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Radota K., Matsuda H.A., Ashburner M., Batalov S., Coavant T.,
A Robi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
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Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Brownstein M.J., Hull D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Iyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Asaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Annothonal annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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-!- SIMILARITY: Contains 1 DAPIN domain. -!- SIMILARITY: Contains 1 CARD domain.

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2 HFVDQYREQLIARVISVEVVLDKIHGQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDRK 61
                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Leukemia;
MEDLINE-Leukemia;
MEDLINE-20036508; PubMed=10567338;
MEDLINE-20036508; PubMed=10567338;
MEDLINE-20036508; PubMed=10567338;
Mikawa N., Hidaka B., Ayukawa K., Higuchi T., Sagara J.;
Nikawa N., Hidaka B., Katsuyama T., Higuchi T., Sagara J.;
"ASC, a novel 22-kDa protein, aggregates during apoptosis of human promyelocytic leukemia HL-60 cells.";
J. Biol. Chem. 274:33835-33838(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vertino P.M., "TMS1, a novel proapoptotic caspase recruitment domain protein, is target of methylation-induced gene silencing in human breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bertin J.;
"CARDS protein is a CARD/PYRIN family member that is involved in apoptosis signal transduction.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASC RUMAN STANDARD; PRT; 195 AA.

4S.

490123; Q96D12; Q9BSZ5; Q9HBD0; Q9NXJ8;

16-0CT-2001 (Rel. 40, Created)

16-0CT-2001 (Rel. 40, Last sequence update)

10-0CT-2003 (Rel. 42, Last annotation update)

Apoptosis-associated speck-like protein containing a CARD (hASC)

(PYCARD) (Target of methylation-induced silencing 1) (Caspase recruitment domain protein 5).

ASC OR TMS1 OR CARD5.
                                                                                                                                                                                                                                                             ;
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SEQUENCE FROM N.A. (ISOFORM 1).
SEQUENCE FROM N.A. TSChopp J.;
Martinon F., Hofmann K., Tschopp J.;
"Pycard a PyD and CARD containing molecule.";
"Pycard a PyD and CARD containing molecule.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                             20; Indels
                                                                                                                                                                            K -> E (IN REF. 3).
2A4EA40194870B31 CRC64;
                                                                                                                                                                                                                         51.6%; Score 253; DB 1;
61.2%; Pred. No. 4.6e-18;
iive 11; Mismatches 20;
            MGD; MGI:1931465; Asc.
GO; GO:0005829; C:cytosol; IDA.
InterPro; IPR001315; CARD.
InterPro; IPR004020; PAAD_DAPIN_dom.
Pfam; PF02758; PAAD_DAPIN; 1.
PROSITE; PS50829; CARD; 1.
Apoptosis; Anti-oncogene.
DOMAIN.
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TISSUE=Fibroblast;
                                                                                                                                                                 CARD.
                                                                                                                                                                                                                                                                                                                                                                                  81
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                                                                                                                                                            105 193 C
159 159 K
193 AA; 21458 MW;
                                                                                                                                                                                                                                                                                                                                                                 62 CKDGLYQALKETHPHLIMEL
                                                                                                                                                                                                                                                                49; Conservative
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                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                              DOMAIN
CONFLICT
SEQUENCE
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use by non-profit institutions as long as its content is in no way additied and this statement is not removed. Usage by and for commercial entities requires a license afreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Inchara N., Nunez G.;
"Genes with homology to mammalian apoptosis regulators identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ie-òcr-2001 (Rel. 40, Created)
16-ocr-2001 (Rel. 40, Last sequence update)
10-ocr-2003 (Rel. 42, Last annotation update)
Apoptosis-associated speck-like protein containing a CARD (PYCARD)
ASC OR ASCL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VSP 004118.
Missing (In isoform 2).
/FTId=VSP 004119.
455987286586F46A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Missing (in isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apoptosis; Anti-oncogene; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0006917; P:induction of apoptosis; TAS.
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                                                                                                                                                                                         AF255794; AAF99665.1;
AF10103; AAG30286.1;
AAR68550.1;
AK000211; BAA91012.1; ALT_FRAME.
BC004470; AAH04470.1;
BC013569; AAH13569.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.2%; Score 236;
                                                                                                                                                                                                                                                                                                                                                                                            InterPro, IPR001315; CARD.
InterPro, IPR04020; PAAD DAPIN dom.
Prom, PP02758; PAAD DAPIN; 1.
PROSITE; PS50209; CARD; 1.
PROSITE; PS50824; DAPIN; 1.
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                                                                                                             EMBL; AB023416; BAA87339.2; -.
EMBL; AF184072; AAC01187.1; -.
FMBL: AF184073; AAG01188.1; -.
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EMBL;
EMBL;
EMBL;
EMBL;
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                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).

SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).

XI STUBELLYMPA, and Pancreas;

MEDLINE=22388257; PubMed=1247,932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

A Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdan T.B., Toshiyuki S., Carrinci P., Frange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernen K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hillyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

"Thuman and mouse cDNA sequences",

"Thuman and mouse cDNA sequences",

"Thuran and mouse cDNA sequences",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isocia—goulz3-3; Sequence=VSP_004118;
Note=No experimental confirmation available;
ISOE SPECIFICITY: Widely expressed at low levels. Detected in peripheral blood leukocytes, lung, small intestine, spleen, thymus, colon and at lower levels in placente, liver and kidney. Very low expression in skeletal muscle, heart and brain. Detected in the leukemia cell lines Hi-60 and U937, but not in Jurkat T-cell lymphoma and Daudh Burkitt's lymphoma. Detected in the melanoma and Daudh Burkitt's lymphoma. Detected in Hele cervical carcinoma cells and Molt 4 lymphocytic leukemia cells. Islencing may affect genes and proteins that act as positive mediators of cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION, AND SUBCELLUTAR LOCATION.
MEDLINE-20552140; PubMed=11103777;
MCCOnnell B.B., Vertino P.M.;
"Activation of a caspase-9-mediated apoptotic pathway by subcellular redistribution of the novel caspase recruitment domain protein TMS1.";
Cancer Res. 60:6243-6247(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       caspase activation,
                       TISSUE=Colon mucosa;
Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: Promotes caspase-mediated apoptosis. This proapoptotic activity is mediated predominantly through the activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          caspase 9.
SUBCELLULAR LOCATION: Cytoplasmic. Upstream of caspase activa a redistribution from the cytoplasm to the aggregates occurs. These appeared as hollow, perinuclear spherical, ball-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains 1 DAPIN domain.
SIMILARITY: Contains 1 CARO domain.
CAUTION: Ref. 5 sequence differs from that shown due to a
frameshift in position 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative_splicing; Named isoforms=3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q9ULZ3-1; Sequence=Displayed;
     (ISOFORM 1).
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ALTERNATIVE PRODUCTS:
     FROM N.A.
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Gaps

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Length 195; 18; Indels

; DB 1; 2.2e-16;

203 AA.

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MEDLINE=21570185; PubMed=11551959;
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CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
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  and for commercial
           (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                  09Y2Ğ2; Q96P82;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Caspase recruitment domain protein 8 (Apoptotic protein NDPP1) (DACAR)
(CARD-inhibitor of NF-kappaB activating ligand) (CARDINAL) (TUCAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang H.;
"A novel apopototic protein, NDPP1, containing CARD and BH3 domains.";
submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                    1 LHFVDQYREQLIARVTSVEVVLDKL-HGQVLSQEQYERVLAENTRPSQMRKLFSLSQSW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99946063; PubNed=10231032;
Nagase T., Ishikawa K.I., Suyama M., Kikuno R., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XII The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 6:63-70(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE=21950691; PubMed=11821383;
Razmara M., Srinivasula S.M., Wang L., Poyet J.-L., Geddes B.J.,
DiStefano P.S., Bertin J., Alnemri B.S.;
"CRRD-8 protein, a new CARD family member that regulates caspase-1
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                              ..
                                                                                                                                                                        19.6%; Score 96; DB 1; Length 203; 31.3%; Pred. No. 0.016; tive 25; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            novel CARD-containing protein."; (JAN-2001) to the EMBL/GenBank/DDBJ databases.
  ζq
                                                                                                                                                     203 AA; ,22867 MW; EF457179EB7A78A7 CRC64;
modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                          431 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activation and apoptosis.";
J. Biol. Chem. 277:13952-13958(2002)
                                                                                                                                                                                                                                                                            GNKGKEVLYDALRESNKFLMDDL 199
                                         EMBL, AF231013, AAF66956.1; -. ZFIN, ZDB-GENB-000511.2; asc1.
InterPro; IPR001315; CARD.
InterPro; IPR004020; PAAD_DAPIN_dom.
Pfam, PF02758; PAAD_DAPIN, 1.
PROSTIE; PS50203; CARD, 1.
PROSTIE; PS50824; DAPIN, 1.
                                                                                                                                                                                                                                                               81
                                                                                                                                DAPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM LONG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM LONG).
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SEQUENCE FROM N.A. (ISOFORM LONG).
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SEQUENCE FROM N.A. (ISOFORM LONG)
                                                                                                                                                                                                                                                               DRKCKDGLYQALKETHPHLIMEL
                                                                                                                                                                                     .larity 31.3%;
Conservative 2
                                                                                                                     Apoptosis; Anti-oncogene.
                                                                                                                                           203
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                                                                                                                                                                                    Local Similarity
Les 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vito P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rissum=Brain:
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                                                                                                                                                                                                                                                                                                                                          HUMAN
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Submitted
                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                               59
                                                                                                                                                                           Query Match
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Matches
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Bouchier-Hayes L., Conroy H., Egan H., Adrain C., Creagh E.M., MacFarlane M., Martin S.J.; "CARDINAL, a novel caspase recruitment domain protein, is an inhibitor of multiple NF-Kappa B activation pathways."; J. Biol. Chem. 276:44069-44077 [2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22062958; PubMed=12067710; Stilo R., Leonardi A., Formisano L., Di Jeso B., Vito P., Liguoro D.; Stilo R., Leonardi A., Formisano L., Di Jeso B., Vito P., Liguoro D.; TUCAN/CARDINAL and DRAL participate in a common pathway for modulation of NF-kappaB activation.", FEBS Lett. 521:165-169(2002).

-!- FUNCTION: Inhibits NF-kappa-B activation. May participate in a regulatory mechanism that coordinates cellular responses controlled by NF-kappa-B transcription factor. Involved in the negative regulation of caspase.

-!- SUBUNIT: May form homodimers. Interacts with NEMO and DRAL. Binds to caspase.], pseudo-ICE and ICEBERG. Interacts with FNBP3 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pathan N., Marusawa H., Krajewska M., Matsuzawa S.-I., Kim H., Okada K., Torii S., Kitada S., Krajewski S., Welsh K., Pio F., Godzik A., Reed J.C.; Caspase-associated recruitment domain family protein overexpressed in cancer."; J. Biol. Chem. 276:32220-32229(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Short,
IsoId=09Y2G2-2; Sequence=VSP 000782, VSP 000783;
-! TISSUE SPECIFICITY: High expression in lung, ovary, testis and placenta. Lower expression in heart, kidney and liver. Also expressed in spleen, lymph node and bone marrow.
-!- SIMILARITY: Contains 1 CARD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L->R INH_BITS HOMODIMER FORMATION.
E -> G (IN REF. 5).
V -> M (IN REF. 5).
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/FTIG=VSp. 000782.
/FTIGHSp. (In isoform Short).
/FTIGHSp. 000783.
                                                                                                                                                                                                                                                                                     Guo J.H., Yu'L.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION, AND MUTAGENESIS OF LEU-366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9Y2G2-1; Sequence=Displayed;
                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM SHORT).
TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21402909; PubMed=11408476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB023172; BAA76799.1; --
EMBL; AF322184; AAG50014.1; --
EMBL; AR331519; AAK01126.1; --
EMBL; AY026325; AAK08982.1; --
EMBL; AF405558; AAA46959.1; --
EMBL; AF511652; AAM46959.1; --
EMBL; AF511652; AAM46959.1; --
INTERPORT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50209; CARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131
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60
326
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                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           366
60
326
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122 S
40246 MW;
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Best Local Similarity 23.09
Matches 23; Conservative
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122 1
349 AA;
                                                                                                                                                                                                           LINI NYCCO
P08548;
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE.
                                                                                                                                                                              RESULT 7
LIN1 NYCCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDILINE=95327607; Pubmed=8672129;

Minterce A.K., Fredholm M., Davies W.;

Minterce A.K., Fredholm M., Davies W.;

Minterce A.K., Fredholm M., Davies W.;

"Evaluation and characterization of a porcine small intestine cDNA

library: analysis of 839 clones.";

Mamm. Genome 7:509-517(1996).

INFECTION: MAY PLAY A ROLE IN MEDIATING RESISTANCE TO VIRUS

-: FUNCTION: MAY PLAY A ROLE IN MEDIATING RESISTANCE TO VIRUS

-: CATALYTIC ACTIVITY: Binds double-stranded RNA and polymerizes ATP

INFECTION: CONTROL OF CELL GROWTH, DIFFERENTIATION, AND APOPTOSIS.

-: CATALYTIC ACTIVITY: Binds double-stranded RNAs into that, when activated, cleaves single-stranded RNAs.

-: SUBGNIT: Homotetramer (S) similarity).

-: SUBGNIT: Homotetramer (S) similarity).

-: SUBCELLULAR LOCATION: ASSOCIATED WITH DIFFERENT SUBCELLULAR FRACTIONS SUCH AS MINICARIA, NUCLEAR, AND ROUGH/SMOOTH MICROSOMAL FRACTIONS (BY SIMILARITY).
                                                                                                                           | : | | | : : | | | : : | | 347 FVKENHRQLQARAKGDLKGVLDDLQDNEVLTENEKELVEQEKTRQSKNEALLSMVEKKGDL 406
                                                                                                        3 FVDQYREQLIARVISVEVVLDKLH-GQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDRK 61
                                                                           1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823,
                                                                                                                                                                                                                                                                                                 TS-DEC-1998 (Rel. 37, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last amnotation update)
21-5/-01/goadenylate synthetase 1 (EC 2.77.-) ((2-5')oligo(A)
synthetase 1) (2-5A synthetase 1) (p42 OAS).
                                         19.3%; Score 94.5; DB 1; Length 431; 32.5%; Pred. No. 0.05; ive 17; Mismatches 36; Indels 1
L -> P (IN REF. 5).
CB54D130807732E6 CRC64;
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InterPro; IPR006117; 25A SYNTH 2.
InterPro; IPR006116; 25A SYNTH 2.
InterPro; IPR00116; 25A SYNTH 2.
INTERPRO; IPR001201; PAP 25A COFE.
PROSITE; PS00832; 25A SYNTH 1; 1.
PROSITE; PS00831; 25A SYNTH 2; 1.
PROSITE; PS0152; 25A SYNTH 3; 1.
RNA-binding; Transferase; Nucleotidyltransferase;
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Thesis (1997), University of Aarhus, Denmark
                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                   407 ALDVLFRSISERDPYLVSYL 426
                                                                                                                                                                 62 CKDGLYQALKETHPHLIMEL 81
422 I
48932 MW;
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                                                         Local Similarity 32.5
les 26; Conservative
                                                                                                                                                                                                                                                                        STANDARD;
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422
431 AA;
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Q29599; O'
CONFLICT
                                            Query Match
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                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nycticebus coucang (Slow loris).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Strepsirhini, Loridae, Nycticebus.
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NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                            44 RPSQMRKLFSLSQSWDRKCKDGLYQALKETH-----PHLIMEL-----WEKGSKK
                                                                                                                                                                                                                                                                                          18;
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                                                                                                                                                      Query Match
15.3%; Score 75; DB 1; Length 349;
Best Local Similarity 32.7%; Pred. No. 3.3;
Matches 18; Conservative 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38; Indels
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SEQUENCE 1260 AA; 147042 MW; 7A6803DF471F7253 CRC64;
S -> R (IN REF. 2).
. 06949A35BFCF7710 CRC64;
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09Y229; 08HWF5;
28-FRE-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
CASPASE recruitment domain protein 4 (Nod1 protein).
CARAB4 OR NOD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 RKCKDG-----LYQALKETHPHLIMELWEKGSKKGLLP
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01-AUG-1988 (Rel. 08, Last sequence update)
01-AUG-1988 (Rel. 08, Last annotation update)
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23.0%; Pred. No. 19;
tive 24; Mismatches
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InterPro; IPR005135; Exo_endo_phos.
InterPro; IPR000477; RVTse.
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TISSUE=Endothelial cells;
MEDLINE=99240667; Pubmed=10224040;
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MUTAGEN
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                                                                                                                                                                                                                                                                                                                         CTISSUB-Lymph,

WEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

METAUSENER R.D., Felingold E.A., Gruse L.H., Derge J.G.,

RIAUSENER R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Mokins R.F., Jordan H., Moore T., Max S.I., Wang J., Habteh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peteras G.J., Abramson R.D., Mullahy S.J.,

Rochards S., Worley K.C., Hale S., Garcia A.M., Gabs R.A.,

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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Hatseley R.W., Touchman J.W., Gremutz M., Marra M.A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

"Thuman and mouse cDNA sequences",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: Self-associates. Binds to caspase-9 and RICK by CARD-CARD interaction.
-!- SUBURLINITEAR LOCATION: Cytoplasmic.
-!- TISSUB SPECIFICITY: Highly expressed in adult heart, skeletal muscle, pancreas, spleen and ovary. Also detected in placenta, lung, liver, kidney, thymus, testis, small intestine and colon.
-!- SIMILARITY: Contains 1 CARD domain.
-!- SIMILARITY: Contains 9 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21264704; PubMed=11058605;
Inohara N., Ogura Y., Chen F.F., Muto A., Nunez G.;
Inohara N. Ogura Y., Chen F.F., Muto A., Nunez G.;
"Human Nod1 confers responsiveness to bacterial lipopolysaccharides.";
J. Biol. Chem. 276:2551-2554(2001).
-!- FUNCTION: Enhances caspase-9-mediated apoptosis. Induces NF-kappa-1-FUNCTION: Enhances caspase-9-mediated apoptosis. Induces NF-kappa-1-FUNCTION: Enhances caspase-9-mediated apoptosis. Induces NF-kappa-1-FUNCTION: RIPE RIPE NF-GENERAL CONFERS responsiveness to intracellular bacterial lipopolysaccharides
Bertin J., Nir W.-J., Fischer C.M., Tayber O.V., Errada P.R., Grant J.R., Keilty J.J., Gosselin M.L., Robison K.E., Wong G.H.W., Glucksmann M.A., Distefano P.S.;

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that activates NF-kappaB.";
J. Biol. Chem. 274:12955-12958(1999).
                                                                                                             SEQUENCE FROM N.A., AND MUTAGENESIS OF VAL-41 AND LYS-208.
TISSUE=Breast;
MEDLINE=99262599; PubMed=10329646;
Inohara N., Koseki T., del Peso L., Hu Y., Yee C., Chen S., Carrio I Merino J., Liu D., Ni J., Nunez G.;
"Medl, an Apaf-1-like activator of caspase-9 and nuclear factor-kappaB.", Chem. 274:14560-14567(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AF126484, AAD29125.1; --
EMBL, AF1364, AAD29225.1; --
EMBL, AF113925, AAD28350.1; --
EMBL, BCG40339; AAH40339.1; --
Genew, HGNC:16390; CARD4.
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PERCURNER FROM N.A.

PERCURNER FROM N.A.

PERCURNER FROM N.A.

STRAIN=NOD; TISSUB=Cerebellum, and Spleen;

STRAIN=NOD; TISSUB=Cerebellum, and Spleen;

STRAIN=NOD; TISSUB=Cerebellum, and Spleen;

MEDLINE=22354683; PubMed=1246681;

A Natado I., Osaton N., Salto R., Suzuki H., Yamanaka I., Kiyosawa H.,

Natado I., Osaton Y., Hasegawa Y., Nogami A., Schonbach C., Golobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Bradt D., Brusic V., Chochia C., Corbani D.E., Cousins S.,

Blake J.A., Bradt D., Brusic V., Chochia C., Corbani D.E., Cousins S.,

Baldarelli R., Gariboldi M., Gissi C., Godzik A., Frazer K.S.,

Garimond S., Gustinoldi M., Gissi C., Godzik A., Gough J.,

Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Magabiima T., Numata K., Okido T., Pavan W.J., Pertea G., Pescle G.,

A Nagashima T., Numata K., Okido T., Pavan W.J., Pertea S.,

Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
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LRR 1.

LRR 3.

LRR 4.

LRR 5.

LRR 6.

LRR 7.

LRR 9.

V-Q: ABOLISHES CASPASE-9 ACTIVATION AND INTERACTION WITH RICK.

K-R: REDUCES CASPASE-9 ACTIVATION.

K-R R -> H (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REQLIARVTSVEVVLDK-LHGQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDRKCKD--
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0A9DF5FC6487E21A CRC64;
GO; GO:0008656; F: caspase activator activity; TAS.

GO; GO:0006915; P: papoptosis; TAS.

GO; GO:000715; P: papoptosis; TAS.

GO; GO:000715; P: papoptosis; TAS.

InterPro; IPRO01315; CARD.

InterPro; IPRO01315; CARD.

READ: PF00619; CARD; I.

READ: PS0619; NACHT; I.

READ: PS06172; NACHT; I.

REPEAT 15 105 CARD; I.

REPEAT 702 209 ATP (POTENTIAL).

REPEAT 702 209 ATP (POTENTIAL).

REPEAT 702 125 LRR 2.

REPEAT 703 LRR 4.

REPEAT 703 LRR 4.

REPEAT 703 LRR 6.

REPEAT 899 862 LRR 6.

REPEAT 899 862 LRR 6.

REPEAT 899 862 LRR 7.

REPEAT 899 862 LRR 8.

REPEAT 891 LRR 9.

REPEAT 892 946 LRR 9.

REPEAT 803 946 LRR 9.

REPEAT 803 946 LRR 9.

REPEAT 803 946 LRR 9.
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CARD.
NACHT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 29.7°,
-hag 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208
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SEQUENCE
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CAR4 MOUSE
LO CAR4 MOUSE
DT 10-OCT
DT
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Read and T. Reed C. C. Red D. C. A. Seton M. Shinada M.,

Bandalin. A. Schnadder C. Serpic C.A. Seton M. Shinada M.,

Bandalin. A. Schnadder C. Serpic C.A. Seton M. Shinada M.,

Werardo M. Wagner L. Wallsteed C. Wang Y. Matanabe Y. Walls C.

By Willing L.G. Whomba Worls A. Wangsteed M. Yang T. Wallsteed S. Mandala M. Sending M. Mandala M. Calling M. Matanabe Y. Wallsteed S. Mandala M. Calling M. Matanabe Y. Matanabe Y. Wallsteed S. Mandala M. Matanabe M. Mandala M. Matanabe Y. Matanabe Y. Matanabe Y. Wallsteed S. Matanabe Y. Matana
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MEDLINE=99098899; PubMed=9880533;
Reboutllat D., Hovnanian A., Marie I., Hovanessian A.G.;
"The 100-Kpa 2', 5'-oligoademylate synthetase catalyzing preferentially the synthesis of dimeric pppA2'p5'A molecules is composed of three
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Muzny D., Arenson A.D., Adams C., Bunac C., Carvelli K., Chang J.,

Chacko J., Chen J., Ding Y., Dugan S., Durbin J., Forcum J.,

Ganesh R., Garcia C., Goodman M., Gorrell J.H., Haywood M.,

Hernandez J., Jackson L., Jin S., Kampal R., Karpathy S., Kovar C.,

Lau S., Leal B., Lee E., Li Y., Jichtarge O., Liu W., Logan O., Lu J.

Ly T., Marondel I., Martinez C., Merscher S., Montgomery K., Oswal G.,

Perez L., Rashid N.D., Renault B., Rowland K., Savage L.,

Scherer S. E., Shen H., Stowall K., Timms K.M., Todd J.,

VO Q., Williamson A., Worley K.C., Yu W., Kucherlapati R., Nelson D.,
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecular basis of T cell-mediated recognition of pancreatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                  Q9Y6K5; Q9H3P5;
16-OCT-2001 (Rel. 40, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
2'-5'-oligoadenylate synthetase 3 (EC 2.7.7.-) ((2-5')oligo(A)
synthetase 3) (2-5A synthetase 3) (pl00 OAS) (pl00OAS) (P/OKCL.4).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21174977; PubMed=11280764;
Ito M., Shichijo S., Tsuda N., Ochi M., Harashima N., Saito N.,
                                                                                                                                                                                     DB 1; Length 953;
                                                                                                                                                                                                               17; Mismatches 38; Indels
                                                                                                                                          107739 MW; 39C639621CEB1A58 CRC64;
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Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1087 AA.
                                                                                                                                                                                   14.7%; Score 72; 26.0%; Pred. No.
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MEDLINE=20564207; PubMed=11112351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cells.";
Cancer Res. 61:2038-2046(2001).
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87 LYVLQQLEDAYVDLRLW 103
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homologous domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens (Human)
Local Similarity
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                                                                                                                             REPEAT
VARIANT
SEQUENCE
                                                                                                                                                                                       Query Match
NP_BIND
REPEAT
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
OAS3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
 0444444444
                                                                                                                                                                                                                                                                    g
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MEDLINE=21357209; PubMed=11463916;
Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
Tettelin H., Nelson K.E., Paulsen I.T., Haft D.H., Dadson R.J.,
Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
"Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 QYREQLIARVTSVEVV-----LDKLHGQVLS--QEQYERVLAENTRPSQMRKLFSLSQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR, SP0244. -..
HAMARP, MF 00049; -: 1.
HIGENOS1025. 1.
INTERPRO1 IPR002300; LRNA-SYNL 1a.
INTERPRO; IPR003100; LRNA-SYNL 1a.
INTERPRO; IPR001412; LRNA-SYNL 1.
INTERPRO; IPR00130; VAIRS_IIERS_edit.
PETM; PR00131; LRNA-SYNTHLEU.
TIGRERAMS; TIGR00396; IRNASYNTHLEU.
TIGRERAMS; TIGR00396; leus_bact, 1.
Aminoacyl-tRNA synthētase, Protein biosynthesis; Ligase, ATP-binding;
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS).
LEUS OR SP0254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.5%; Score 71; DB 1; Length 833; 25.3%; Pred. No. 22; tive 21; Mismatches 38; Indels
                                                 Streptococcus pneumoniae.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "HIGH" REGION.
"KMSKS" REGION.
ATP (BY SIMILARITY).
7CAA4FB5B4F99EB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 WDRKCKD---GLYQALKETHPHLIMELWEKGSKKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 40, Created)
(Rel. 40, Last seq
(Rel. 43, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE007338; AAK74433.1; -. PIR; H95029; H95029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             833 AA; 94421 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 25...
Best 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52
614
613
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Q60856;
16-OCT-2001
16-OCT-2001
15-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DASB_MOUSE
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             ò
                                       RMEL; AF063613; AAD288543.1; --
REMEL; AB044455; BAB18647.1; --
REMEL; AB044455; BAB18647.1; --
REMEL; AB044455; BAB18647.1; --
REMEL; AC04551; -; NOT_ANNOTATED_CDS.
REMEL; AF251351; -; NOT_ANNOTATED_CDS.
REMEL; AF251351; -; NOT_ANNOTATED_CDS.
REMEL; AF251351; -; NOT_ANNOTATED_CDS.
REMEL; AF251351; -; NOT_ANNOTATED_CDS.
REMEL; AF36788; OAS3-ANTH_2.
REMEL; PRO065139; PRO065117; 25A_SYNTH_2.
REPTO; IPRO06116; 25A_SYNTH_2.
REPTO; IPRO01201; PAP_25A_COPE.
REMEL; PRO01301; PAP_25A_COPE.
REMEL; PRO01301; PAP_25A_COPE.
REMEL; PRO01301; PAP_25A_COPE.
REMEL; PRO01303; 25A_SYNTH_1; 2.
REMEL; REMEMEL; REMEMEL; REMEMEL; REMEMEL; REMEMEL; REMEMENTER; REMEMER; REMEMENTER; REMEMER; REM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 NTRPSOMRKLFSLSQSW-DRKCKDGLYQALKETHPHL-IMEL-----WEKGSKKGLLPLS 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Pred. No. 23;
11; Mismatches 18; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OAS DOMAIN 1.
LINKER.
OAS DOMAIN 2.
OAS DOMAIN 3.
R -> K (IN REF. 2).
G -> A (IN REF. 1).
A -> G (IN REF. 1).
CL -> HV (IN REF. 1).
GL -> HV (IN REF. 1).
GAASIV -> AEPASY (IN REF. 1).
HV -> QL (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.7%; Score 72; DB 1; Length 1087; 35.0%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121164 MW; 3DABED08FB08AEBA CRC64;
        Rebouillat D., Hovnanian A., David G., Hovanessian A.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 39
503
984 98
1087 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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Best Local Simil
Matches 21; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-OCT-2003
10-OCT-2003
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYL STRPN
Q978s0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
SYL STRPN
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44443

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144-150; 154-176; 208-217; 251-258; 273-284; 337-352; 374-380; 383-389; 448-456 AND 459-479.
TISSUE-Gizzard, and Skeletal muscle;
MEDLINE-97150869; PubMed-8995405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54402 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 36.4
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gizzard smooth muscle.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11
174 1
494 AA;
                                                                                                                                                                     Kirley T.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OAS1 OR OIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INIT MET
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
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OAS1_HUNAN

AC 000873;

AC 026.073;

DT 16-0CT-

DT 16-0CT-

DT 15-0CT-

DT 15-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                    % THE TETT T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -I-CATALTIC ACTIVITY: Binds double-stranded RNA and polymerizes ATP into PPP(A2'PS'A)N oligomers, which activate the latent RNase L that, when activated, cleaves single-stranded RNAs.

-I-SIMILARITY: Belongs to the 2-5A synthetase family.

-I-SIMILARITY: Belongs to the 2-5A synthetase family.

-I-SIMILARITY: Belongs to the Book of through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>.</u>.
                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91232962; PubMed=1709495; Rutherford M.N., Kumar A., Nissim A., Chebath J., Williams B.R.G.; Wither murine 2-5A synthetase locus: three distinct transcripts from two linked genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 19:1917-1924 (1991).
-!- FUNCTION: THE 2-5A SYSTEM (THE OASS, 2-5A, AND RNASE L) MAY PLAY ROLE IN MEDIATING RESISTANCE TO VIRUS INFECTION, CONTROL OF CELL GROWTH, DIFFERENTIATION, AND APOPTOSIS.
                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 1-21; 68-73; 83-90; 108; 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 NTRPSQMRKLFSLSQSWDRKCKDGLYQALKETHPHLIMEL----WEKGSK 87
            2'-5'-oligoadenylate synthetase 1B (EC 2.7.7.-) ((2-5')oligo(A) synthetase 1b) (2-5A synthetase 1B) (Fragment). OAS1B OR OIAS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 2 (EC 3.6.1.3)
(NTPDase2) (Ecto-ATPase) (CD39 antigen-like 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S15661; S1661.

MGD; MG1: 97430; Oaslb.

GO; GO:0003800; F:antiviral response protein activity; IDA.
InterPro; IPR006117; 25A_SYNTH_2.
InterPro; IPR006116; 25A_SYNTH_2.
InterPro; IPR0011201; PAPP 25A_COTE.
PROSITE; PS00832; 25A_SYNTH_1; PARTIAL.
PROSITE; PS00833; 25A_SYNTH_1; PARTIAL.
PROSITE; PS50123; 25A_SYNTH_1; PARTIAL.
PROSITE; PS50123; 25A_SYNTH_3; IPARTIAL.
PROSITE; PS50123; 25A_SYNTH_3; IPARTIAL.
PROSITE; PS50123; 25A_SYNTH_3; IPARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.3%; Score 70; DB 1; Length 192; 33.3%; Pred. No. 5.4; ive 9; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 192
192 AA; 21936 MW; 4ElCOllEF9024F46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               494 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X55982; CAA39455.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NTPDase2) (Ecto-ATPase)
ENTPD2 OR CD39L1.
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interferon induction.
                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
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P79784;
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SEQUENCE
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ENP2_CHICK
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"Complementary DNA cloning and sequencing of the chicken muscle ecto-ATPase. Homology with the lymphoid cell activation antigen CD39."; J. Biol. Chem. 272:1076-1081(1997).
                                                                                                                                                                                                                                                                                                                                                               912.221 smooth mustire.;

1. Biochem. Biophys. Methods 29:61-75(1994).

1. FUNCTION: In the nervous system, could hydrolyze ATP and other nucleotides to regulate purinergic neurotransmission. Hydrolyzes ADP only to a marginal extent (By similarity).

1. CATALYTIC ACTIVITY: ATP + H(2)0 = ADP + phosphate.

1. COFACTOR: Requires calcium and magnesium.

1. SUBCELLULAR LOCATION: Integral membrane protein (Potential).

1. PTM: Has probably disulfide bonds.

1. SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                               MEDINE=95081479; PubMed=7989647;
Stout J.G., Kirley T.L.;
"Purification and characterization of the ecto-Mg-ATPase of chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-LEU
N-LINKED (GLCNAC. . .) (POTENTIAL).
L -> LL (IN REF. 2).
ENF -> GNK (IN REF. 2).
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P00973; P04820; P29080; P29081; P78485; P78486; Q16700; Q16701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last amnotation update)
27-57-01jgoademylate synthetase 1 (EC 2.7.7.-) ((2-5')oligo(A) synthetase 1) (2-5A synthetase 1) (p46/p42 OAS) (E18/E16).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, U74467, AAC60071.1; -.
InterPro, IPR00407; GDA1_CD39_NTPase.
Plan; PF01150; GDA1_CD39, 1.
PR051TE; PS01228; GDA1_CD39 NTPASE; 1.
Hydrolase; Transmembrane; Glycoprotein; Calcium; Magnesium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 70; DB 1; Length 494;
Pred. No. 15;
7; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 VLKRLLSKVLQABNYQETVANPCWPTGYRKSLSLSLSSIYDSPCTE 287
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                         SEQUENCE OF 1-12 AND 154-176, AND CHARACTERIZATION
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A REDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Gruse L.H., Derge J.G.,

RA Altaschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Habieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,

RA Roha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pilalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

RA Mitting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

RA Blakesley R.W., Touchman J.W., Grene E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Grene E.D., Dickson M.C.,

RA Schnerch A., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

RI Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muzny D., Arenson A.D., Adams C., Bunac C., Carvelli K., Chang J., Chacko J., Chen J., Ding Y., Dugan S., Durbin J., Forcum J., Gancia C., Goodman M., Gorrell J.H., Haywood M., Hernandez J., Jackson L., Jin S., Kampal R., Karpathy S., Kovar C., Lau S., Leal B., Lee E., Li Y., Lichtarge O., Liu W., Logan O., Lu J. Y., Marondel I., Martinez C., Merscher S., Montgomery K., Oswal G., Perez L., Rashid N.D., Renault B., Rowland K., Savage L., Scherer S.E., Shen H., Simon M., Stovall K., Timms K.M., Todd J., Vo Q., Williamson A., Worley K.C., Yu W., Kucherlapati R., Nelson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning, sequencing, and expression of two murine 2'-5'-oligoadenylate synthetases. Structure-function relationships."; J. Biol. Chem. 266:15293-15299(1991).
                                                                                                                                                                                                                                                                                                                  MEDLINE=86108911; PubMed=3753689; Wathelet M.G., Moutschen S., Cravador A., Dewit L., Defilippi P., Huez G.A., Content J.; Hull-length sequence and expression of the 42 kDa 2-5A synthetase induced by human interferon."; FEBS Lett. 196:113-120(1986).
                                                                                                                              ď
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                              oligo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 곲
                                                                      SEQUENCE FROM N.A. (ISOFORMS P41 AND P46).
MEDLINE=86081732; PubMed=2416561;
Benech P., Mory Y., Revel M., Chebath J.;
"Structure of two forms of the interferon-induced (2'-5') oligosynthetase of human cells based on cDNAs and gene sequences.";
EMBO J. 4:2249-2256(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS P48 AND P41).
MEDLINE=91332052; PubMed=1651324;
Ghosh S.K., Kusari J., Bandyopadhyay S.K., Samanta H., Kumar
                                                                                                                                                                                                                                        Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM P41).
MEDLINE=86223945; PubMed=3754863;
Shiojiri S., Fukunaga R., Ichii Y., Sokawa Y.;
"Structure and expression of a cloned cDNA for human S.)oligoadenylate synthetase.";
J. Dilgoadenylate synthetase.";
J. Biochem. 99:1455-1464(1986).
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SEQUENCE OF 255-364 FROM N.A. (ISOFORM P41).
MEDLINE=83273721; PubMed=6348777;
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J. BIOL. Chem. 274:25535-25542(1999)

-1. FUNCTION: MAY PLAY A ROLE IN MEDIATING RESISTANCE TO VIRUS

-1. FUNCTION: CONTROL OF CELL GROWTH, DIFFERENTIATION, AND APOPTOSIS.

-1. CATALYTIC ACTIVITY: Binds double-stranded RNA and polymerizes ATP into PPP(A2'P5'A)N oligomers, which activate the latent RNase L that, when activated, cleaves single-stranded RNAs.

-1. SUBUNIT: Homotetramer.

-1. SUBUNIT: Homotetramer.

-1. SUBCELLULAR LOCATION: ASSOCIATED WITH DIFFERENT SUBCELLULAR FRACTIONS BUTCH DIFFERENT SUBCELLULAR PRACTIONS.

-1. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=p48; Synonyms=9-2;
IsoId=P00373-3; Sequence=VSP_003740;
-!- INDUCTION: By interferons.
-!- SIMILARITY: Belongs to the 2-5A synthetase family.
-!- CAUTION: Ref. 8 sequence differs from that shown due to a frameshift in position 400.
-!- CAUTION: Ref. 4 sequence was originally thought to originate from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-88283644; PubMed=2456211;
Rutherford M.N., Hannigan G.E., Williams B.R.G.;
"Interferon-induced binding of nuclear factors to promoter elements of the 2-5A synthetase gene.";
EMBO J. 7:751-759(1988).
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MEDLINE=98070528; PubMed=9407111;
Ghosh A., Sarkar S.N., Guo W., Bandyopadhyay S., Sen G.C.;
"Enzymatic activity of 2'-5'-oligoadenylate synthetase is impaired specific mutations that affect oligomerization of the protein.";
J. Biol. Chem. 272:33220-33226(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-28 FROM N.A.
MEDLINE-88082760; PubMed=3121313;
Wathelet M.G., Clauss I.M., Nols C.B., Content J., Huez G.A.;
Wathelet m.G., Clauss I.M., Nols C.B., Content J., Huez G.A.;
Whew inducers revealed by the promoter sequence analysis of two
interferon-activated human genes.";
Eur. J. Biochem. 169:313-321(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Benech P., Vigneron M., Peretz D., Revel M., Chebath J.;
"Interferon-responsive regulatory elements in the promoter of human 2',5'-oligo(A) synthetase gene.";
Mol. Cell. Biol. 7:4498-4504(1987).
Merlin G., Chebath J., Benech P., Metz R., Revel M.; "Molecular cloning and sequence of partial CDNA for interferon-induced (2'-5')oligo(A) synthetase mRNA from human
                                                                                                                                                                                                                                                                                                                                                                   Saunders M.E., Gewert D.R., Tugwell M.E., McMahon M., Williams B.R.G., "Human 2-5A synthetase: characterization of a novel cDNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUTAGENESIS OF ASP-75 AND ASP-77.
MEDLINE=99395121; PubMed=10464285;
Sarkar S.N., Ghosh A., Wang H.W., Sung S.S., Sen G.C.;
"The nature of the catalytic domain of 2'-5'-oligoadenylate
                                                                                                                                                                                                                                                     SEQUENCE OF 231-400 FROM N.A. (ISOFORM P41), AND INDUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event-Alternative splicing; Named isoforms=3;
Name=p46; Synonyms=46 kDa, E18;
Isofd=p00973-1; Sequence=Displayed;
Name=p41; Synonyms=41 kDa, E16, 3-9;
Isofd=p00973-2; Sequence=VSP_003738, VSP_003739;
                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 80:4904-4908(1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88142842; PubMed=2830497;
                                                                                                                                                                                                                                                                                                 TISSUE=Lymphoblast;
MEDLINE=85284966; PubMed=2411547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           corresponding gene structure.";
EMBO J. 4:1761-1768(1985).
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                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=21452045; PubMed=11544234;
HOSKINS J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S.,
BOBHOFF B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leucyl-ENMA synthetase (EC 6.1.1.4) (Leucine--ERNA ligase) (LeuRS).
LEUS OR SPR0215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 RPIKLKSLIRLVKHWYQNCK----KKLGKLPPQYALELLTVYAWERGSMK 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA binding; Transferase; Nucleotidyltransferase;
Interferon induction; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 833 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC004551; -; NOT ANNOTATED CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X02661; CAA26497.1; ALT_FRAME.
X06500; CAA28493.1; -. ____X0179; CANA.
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AAA39857.1; ALT INIT.
                                                                                                                                                                                                                                                                                                                                                                                          , M11805, AAB59552.1; JOINED.
M11806, AAB59552.1; JOINED.
M11807, AAB59552.1; JOINED.
M11810, AAB59552.1; JOINED.
M11810, AAB59532.1; -...
mouse but is a human sequence
                                                                                                                                                                                                                                                                                                    EMBL; X02875; CAA26634.1; -. EMBL; X02874; CAA26633.1; -.
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                                                                                                                                                                                                                                                                                                                                                                 AAB59552.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAB51602.1;
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PIR; A91013; SYHU16.
PIR; B24359; SYHU18.
Genew; HGNC:8086; OAS1.
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Best Local Similarity
Matches 16; Conserv
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OBDRB6;
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EMBL;
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EMBL;
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AC 89YL
BY 10-0C
BY
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RA Glass J.I.;

Genome of the bacterium Streptococcus pneumoniae strain R6.";

J. Bacteriol. 183:5709-5717(2001)

Glabosphate + L-leucyl-tRNA(Leu) = AMP +

diphosphate + L-leucyl-tRNA(Leu).

Glabosphate + L-leucyl-tRNA(Leu).

Glabosphate + L-leucyl-tRNA(Leu).

Glabosphate + L-leucyl-tRNA(Leu).

Glass-I aminoacyl-tRNA synthetase family.

Glass-I aminoacyl-tRNA synthetase family.

Grass-I synts-RROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BNEL outstation.

Che European Bioinformatics Institute. There are no restrictions on its the Burpean Bioinformatics as long as its content is in no way modified and this statement is not removed. Usage by and for commercial centities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEAMAP ME 00049; -; 1.
InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR001302; Leu-tRNAsyntla.
InterPro; IPR001412; tRNA-synt_1a.
InterPro; IPR001412; tRNA-synt_1i-interPro; IPR001408; ValkS_lieRs_edit.
Pffam; PR00133; tRNA-synt_1i_1.
PRINTS; PR00985; TRNA-SYNTHLEU.
TIGRRAMS; TIGR00396; leus bact; 1.
PROSTIE; PS00178; AA TRNA, Bact; 1.
Aminpacyl-tRNA synthētase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
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ATP (BY SIMILARITY).
53BA80978AB019B9 CRC64;
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833 AA; 94366 MW;
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614
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hypothetical prote
hypothetical prote
retrovitus-related
(2'-5')oligo(A) sy
hypothetical prote
leucyl-tRNA synthe
(2'-5')oligo(A) sy
hypothetical prote
probable myosin he
(2'-5')oligo(A) sy
(2'-5')oligo(A) sy
(2'-5')oligo(A) sy
(2'-5')oligo(A) sy
(2'-5')oligo(A) sy
(2'-5')oligo(A) sy
nuclear phosphopro
nuclear phosphopro
nuclear phosphopro
nuclear phosphopro
nonstructural prot
nonstructural prote
hypothetical prote
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hypothetical prote
hypothetical prote
                                              July 28, 2004, 08:50:22; Search time 13.7349 Seconds (without alignments) 665.325 Million cell updates/sec
                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                         Description
                                                                             US-09-996-617-2_COPY_1335_1429
490
1_LHFVDQYREQLIARVTSVEV........HLIMELWEKGSKKGLLPLSS
                                                                                                                                                       283366
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                       283366 segs, 96191526 residues
                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                        T17255
AB2215
AB2215
GNLRL1
SYMSO2
CN1009
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S15661
B84730
SYHU16
SYKHU16
SYKHU16
SYKHU16
C72238
T1305674
T130574
MNNZ35
MNNZ35
MNNZ35
MNNZ35
T48836
T48836
T48836
T48836
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Query
Score Match Length DB
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
                                                                                                                Scoring table:
                                OM protein
                                                                                                                                                                                                                                 Database :
                                                                                                 Sequence:
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					4	ALIGNMENTS	
 RESULT 1 '117255 hypothetical protein DKFZp5 C;Spcies: Homo sapiens (ma C;Date: 15-0ct-1999 #sequen C;Accession: 171255 R;Koehrer, K.; Beyer, A.; R;Koehrer, K.; Beyer, A.; A;Reference number: 218722 A;Reference number: 218722 A;Accession: 171255 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-1192 *KOE> A;Cross-references: EMBL:ALA A;Experimental source: adult C;Genetics: A;Note: DKFZp58601822.1	tical pression trical pression. Treer, K.; ed to treer out sion. Treer, W.; ed to treer out sion. Treer in treer trimental imental incs:	protein Di mo sapiens tt-1999 #sst 17255 # 17255 the Protei umber: 218 liminary Ppe: mRAA Ppe: mRAA -119 «KAA 1 source: EMI	111 GG CE 111	586018 an) nce_re equenc equenc	22.1 visio H.W. e Dat	- human (fragment) n 15-Oct-1999 #text_c; Gassenhuber, J.; Wi abase, September 1999 clone DKFZp58601822	hange 15-Осt-1999 ещапп, S.
 Query N Best Lo Matches	fatch ocal s 9	C	100.0%; ilarity 100.0%; Conservative	*0.0	SC Pr	Score 490; DB 2; Length Pred. No. 9.5e-41; Mismatches 0; Indels	h 1192; 1s 0; Gaps 0;
Oy Dp		LHFVDQYR; LHFVDQYR]	EQLIARY EQLIARY	71.SV 	EVVLD	R — R	SOMRKLFSLSOSWDR 60
& 42	61 1	KCKOGLYQ. 	ALKETHI ALKETHI	ğ=ğ	MELWE MELWE	KCKDGLYQALKETHPRLIMELWEKGSKKGLLPLSS 95 	
RESULT 2 AB2515 hypothetical protein alr7298 [imported hypothetical protein alr7298 [imported c) Species: Nostoc sp. PCC 7120 A,Note: Nostoc sp. strain PCC 7120 is C,Date: 14-Dec 2001 #sequence_revision c,Accession: AB2115 R,Kaneko, T.; Nakamura, Y.; Wolk, C.P. Nakazaki, N.; Shimpo, S.; Sugimoto, IDNA Res. 8, 205-213, 2001 A,Title: Complete Genomic Sequence of A,Reference number: AB1807; MUID:21599 A,Accession: AB2515 A,Status: preliminary A,Molecule type: DNA A,Residues: 1-492 *KUR> A,Residues: 1-492 *KUR> A,Residues: 1-492 *KUR> A,Genetics: alr7298 A,Genetics: alr7298 A,Genetics: alr7298	trical press Nostoc Nostoc 14-Dec 14-Dec 16-Dec 16-	ABSS15 ABSS16 ABSS16 ABSS16 C)Species: Nostoc sp. P A,Note: Nostoc sp. stra C,Date: 14-Dec-2001 #se C,Accession: ABSS15 A,Kaneko, T.; Nakamura, Nakazaki, N.; Shimpo, DNA Res. 8, 205-213, 20 A,Title: Complete Genom A,Reference number: AB1 A,Recerence number: AB1 A,Residues: 1-482 × KRNS A,Residue	lr7298 PCC 71; ain PCC equence ' Y.; V S.; Si mic Sec 1807; h :BA000C	[im 20 77 71 71 19 19 19 19 19 19 19 19 19 19 19 19 19	[imported] 20 20 C 7120 is a e_revision Wolk, C.P.; ugimoto, M. quence of t MUID:215952	i) - Nostoc sp. a synonym of An 14-Dec-2001 #t ; Kuritz, T ; S M.; Takazawa, M. the Filamentous 5285; PMID:11759	(strain PCC 7120) plasmid pCC7120a. abaena sp. strain PCC 7120 ext_change 09-Dec-2002 asamoto, S.; Watanabe, A.; Iriguch ; Yamada, M.; Yasuda, M.; Tabata, Nitrogen-fixing Cyanobacterium An. 840

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C;Accession: A39417
R;Ghosh, S.K.; Kusari, J.; Bandyopadhyay, S.K.; Samanta, H.; Kumar, R.; Sen, G.C.
A; Biol. Chem. 266, 15293-15299, 1991
A;Title: Cloning, sequencing, and expression of two murine 2'-5'-oligoadenylate syntheta A;Reference number: A39417; MUID:91332052; PMID:1651324
A;Accession: A39417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein PH1337 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Accession: C71005
C;Accession: C71005
R;Kawarabayasi, Y; Sawada, M; Horikawa, H; Haikawa, Y; Hino, Y; Yamamoto, S.; Sekin M; Ohfuku, Y; Punahashi, T; Tanaka, T; Kudoh, Y; Yamazaki, J; Kushida, N; Oguchi M; Ohfuku, Y; Punahashi, T; Tanaka, T; Kudoh, Y; Yamazaki, J; Kushida, N; Oguchi M; Phises: S, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Accession: C71005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-197 <KAW>
A;Cross-references: GB:AP000006; NID:g3236133; PIDN:BAA30443.1; PID:d1031386; PID:g32577
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Residues: 1-363 <GHO>
A, Residues: 1-363 <GHO>
A, Cross-references: GB:M63849
A, Obtoe: the authors translated the codon TTG for residue 259 as Arg
C, Comment: This enzyme, one of those induced by interferons, binds double-stranded RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 LDQLTGSYKPNPQIYVKLIBECTDLQKEGEFSTCFTELQRDFLKQRPTKLKSLIKLVKHW 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 DIWEEKVKEAKKSLRLLKYFIAĞIVGILAVİALLMVYTGYPIIİLGL------ĞLLPLA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Status: preliminary, nucleic acid sequence not shown; translation not shown A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 HFVDQYREQLIARVTSVEVVLDXLHGQVL-SQEQYERVLAENTRPSQMRKLFS----LS 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 HIAHESAEDMİRIISSMDAERAKLRGEVVYHODDWDLLIRERIRKGKRHTAFDFYNPILL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 QSWDRXCKD------GLYQALKET-----HPHLIMELWEKGSKKGLLPLS 94
                                                                                                                                                                                       (2'-5')oligo(A) synthetase (EC 2.7.7.-) 2 - mouse
NiAlternate names: 2'-5'-oligoadenylate synthetase 2
C;Species: Mus musculus (house mouse)
C;Species: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
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14.9%; Score 73; DB 1; Length 363;
Best Local Similarity 25.3%; Pred. No. 9.9;
Matches 24; Conservative 14; Mismatches 25; Indels
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466 KKKSPGPDGFTSEFYQTFKEELVPILLNLFQNIEKEGILP 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 YONCK----KKLGKLPPQYALELLTVYAWERGSMK 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C, Superfamily: oligo (A) synthetase C, Keywords: nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 22.5
Matches 27; Conservative
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GUNELL

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GUNELL

C. Beroirus-related reverse transcriptase pseudogene - slow loris

C. Species: Nycticebus coucang (slow loris)

C. Jate: 31-Mar-1988 #sequence_revision 04-Jan-1996 #text_change 14-May-1999

C. Accession: B25313

R. Hattori, M.; Kuhara, S.; Takenaka, O.; Sakaki, Y.

Nature 321, 625-628, 1986

A. Attale: L. family of repetitive DNA sequences in primates may be derived from a sequence A. Reference number: A93381; MUID:86230917; PMID:2423883

A. Accession: B25313

A. Status: conceptual translation of pseudogene

A. Molecule type: DNA

A. Residues: 1-1260 -HAT>

A. Note: this sequence was constructed from an alignment of six sequences, determined by C. Keywords: reverse transcriptase; pseudogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein Cj1679 [imported] - Campylobacter jejuni (strain NCTC 11168)
C,Species: Campylobacter jejuni
C,Species: Campylobacter jejuni
C,Species: J-Max-2000 #sequence_revision 31-Max-2000 #text_change 03-Jun-2002
C,Accession: D81265
R,Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
Rature 403, 665-668, 2000
A,Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp.
A,Reference number: A81250; MUD:20150912; PMID:10688204
A,Recession: D81265
A,Status: preliminary
A,Residues: 1-584 <PAR>
A,Cross-references: GB:AL139079; GB:AL11168; NID:g6968971; PIDN:CAB73666.1; PID:g696909
C,Genetics:
A,Genetics:
A,Genetics:
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                                                                                                                                                                15 VTSVEVVLDKLHGQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDRKCKDGLYQALKETH
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                                          Length 482;
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                                                                                                     35; Indels
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                                             DB 2;
                                       Query Match
15.3%; Score 75; DB 2
Best Local Similarity 24.1%; Pred. No. 8.8;
Matches 21; Conservative 21; Mismatches
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larity 23.0%; Pred. No. 38;
Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                              315 AGCIVEITATLGQYLSPGNRLGTLQIS 341
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Best Local Similarity
Matches 26; Conserve
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C;Accession: D90592
R;Chambaud, I.; Heillg, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: D90592
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-61 «XUR»
A;Cross-references: GB:AL445566; PID:g14090059; PIDN:CACI3817.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Genetics:

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C; Species: Arabidopsis thaliana (mouse-ear crees)
C; Date: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 02-Peb-2001
C; Accession: F84730
C; Accession: F84730
M; Koo, H; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Fallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Recession: F84730
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Engly (1, 249-2256, 1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985) (1985
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A,Molecule type: DNA
A,Residues: 1.1269 <55TO>
A,Cross-references: GB:AB002093; NID:g6598483; PIDN:AAC69932.2;
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14.3%; Score 70; DB 2;
Best Local Similarity 20.8%; Pred. No. 42;
Matches 25; Conservative 21; Mismatches 34
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C,Superfamily: pullulanase type debranching
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Best Local Similarity 29.2%
Matches 26; Conservative
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D90592
hypothetical protein MYPU_6440 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C,Species: Mycoplasma pulmonis
C,Species: 24-May-2001 #sequence_revision 24-May-2001 #text_change 22-Jun-2003
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: 815661; 819108
R; Rutherford, M.N.; Rumar, A.; Nissim, A.; Chebath, J.; Williams, B.R.G.
Nucleic Acids Res. 19, 1917-1924, 1991
A; Reference number: 81560; MUID: 91232962; PMID: 1709495
A; Accession: 815661
A; Residues: 1-192 «RUTA
A; Residues: 1-192 «RUTA
A; Residues: BRBL: X55982
R; Williams, B.
Submitted to the EMBL Data Library, September 1990
A; Reference number: 819108
A; Accession: 819108
A; Accession: 819108
A; Molecule type: mRNA
A; Residues: 1-175, L', 177-192 «WILA
A; Residues: 1-175, L', 177-192 «WILA
A; Cross-references: EMBL: X55982; NID: 949714; PIDN: CAA39455.1; PID: 949715
C; Superfamily: oligo(A) synthetase
C; Keywords: nucleotidyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 QYREQLIARVISVEVV-----LDKLHGQVLS--QEQYERVLAENTRPSQMRKLFSLSQS 57
                                                                                                                                                leucyl-tRNA synthetase [imported] - Streptococcus pneumoniae (strain TIGR4)
C,Species: Streptococcus pneumoniae
C,Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 NTRPSQMRKLFSLSQSWDRKCKDGLYQALKETHPHLIMEL-----WEKGSK 87
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llarity 33.3%; Pred. No. 9.3;
Conservative 9; Mismatches 17; Indels
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Matches 17; Conserv
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Best Local S:
Matches 24
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A; Molecule type: mRNA
A; Residues: 231-459 sSAU>
A; Residues: 231-459 sSAU>
A; Residues: 231-459 sSAU>
A; Crosex-references: GB: NO2661; NID: g23795; PIDN: CAA26497.1; PID: g1335008
A; Experimental source: interferon-induced baudi lymphoblastoid cells
B; Benech, P.; Mory, Y.; Revel, M.; Chebath, J.
B; Renech, P.; Mory, Y.; Revel, M.; Chebath, J.
A; Title: Structure of two forms of the interferon-induced (2'-5') oligo A synthetase of A; Reference number: A91013; MUID: 86081732; PMID: 2416561
A; Accession: A91013
A; Molecule type: mRNA
A; Residues: 1-346, VRPPASSIPPIPAPLHEA' <BBN>
A; Residues: 1-346, VRPPASSIPPIPAPLHEA' <BBN>
A; Cross-references: GB: X02874; GB: K00006; NID: g35122; PIDN: CAA26633.1; PID: g35123
C; Comment: This enzyme, one of those induced by interferons, binds double-stranded RNA a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cybate: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999
Apcession: B39417
Righosh, S. K.; Kusari, J.; Bandyopadhyay, S.K.; Samanta, H.; Kumar, R.; Sen, G.C.
J. Biol. Chem. 266, 15293-15299, 1991
A.Fitle: Cloning, sequencing, and expression of two murine 2'-5'-oligoadenylate syntheta A;Reference number: A39417; MUID:91332052; PMID:1651324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Title: Human 2-5A synthetase: characterization of a novel cDNA and corresponding gene A,Reference number: A22842; MUID:85284966; PMID:2411547 A,Accession: A22842
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A,Residues: 1-414 <GHO-N
A,Cross-references: GHO-N61850; NID:g200136; PIDN:AAA39858.1; PID:g200137
A,Note: the authors translated the codon TTG for residue 259 as Arg
C;Comment: This enzyme, one of those induced by interferons, binds double-stranded RNA
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C;Date: 20-Aug-1987 #sequence_revision 20-Apr-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                            Gaps
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   For alternate splice forms, see PIR:SYHU16 and PIR:A22842.
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                                                                                                                                                                                                                                                                                                         DB 1; Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 RPSQMRKLFSLSQSWDRKCKDGLYQALKETHPHLIMEL-----WEKGSKK
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                                                                                                          A;Cross-references: GDB:119465; OMIM:164350
A;Map position: 12pter-12qter
C;Superfamily: oligo(A) synthetase
C;Keywords: alternative splicing; nucleotidyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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Best Local Similarity 32.0%; Pred. No. 25;
Matches 16; Conservative 10; Mismatches
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32.0%; Pred. No. 26;
tive 10; Mismatches
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Best Local Similarity 32.03
Matches 16; Conservative
                                                                               A; Gene: GDB:OIAS
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                                                   Nalternate names: oligoadenylate synthetase (EC 2.7.7.-), splice form EI8 - human (2'-5') oligo(A) synthetase (EC 2.7.7.-), splice form EI8 - human (5') oligo(A) synthetase (EC 2.7.7.-), splice form EI8 - human (5') oligo adenylate synthetase (5') oligo adens (1') oligo adens (
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A)Cross-references: GB-M18099, NID:g189326; PIDN:AAA59955.1; PID:g553604
A)Cross-references: GB-M18099, NID:g189326; PIDN:AA59955.1; PID:g553604
B/Wathelet, M.G.; Clauss, I.M.; Nols, C.B.; Content, J.; Huez, G.A.

Eur. J. Blochem. 169, 313-21, 1987
A)Title: New inducers revealed by the promoter sequence analysis of two interferon-active A, Reference number: I37997; MUID:88082760; PMID:3121313
A)Accession: 137997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Comment: For alternate splice forms, see PIR:SYHU18 and PIR:A22842.
C;Genetics:
A;Gene: GDB:OlAS
A;Cross-references: GDB:119465; OMIM:164350
A;Amp position: 12ptcr-12qter
C;Superfamily: oligo(A) synthetase
C;Superfamily: oligo(A) synthetase
C;Reywords: alternative splicing; nucleotidyltransferase
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Reference number: A91013; MUID:86081732; PMID:2416561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.2%; Score 69.5; I
32.0%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Best Local Similarity
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A; Residues: 1-28 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 2-28 <RE
                                       Accession: A91013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
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δ g .. N

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nuclear phosphoprotein xnf7 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Species: 31-pec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jan-2000
C;Accession: A43906; S27947
E;Reddy, B.A.; Kloc, M.; Etkin, L.
Dev. Biol. 148, 107-116, 1991
A;Teference number: A43906; MUID:92038424; PMID:1936552
A;Accession: A43906
A;Accession: A43906.
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A, Residues: 1-609 < RED>
A, Residues: 1-609 < RED>
A, Across-references: EMBL: M63705, NID: 9214914; PID: 9214915
A, Note: sequence extracted from NCBI backbone (NCBIN: 64515, NCBIP: 64520)
C, Genetics:
A, Gene: xnf7
C, Superfamily: Xenopus nuclear phosphoprotein xnf7, RING finger homology
C, Keywords: DNA binding; nucleus; phosphoprotein; zinc finger
F, 141-190/Domain: RING finger homology < RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                 201 RPIKLKSLIRLVKHWYQNCK----KKLGKLPPQYALELLTVYAWERGSMK 246
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თ
                                                                                                                                                                                                                                                                                                                                                                     44 RPSQMRKLFSLSQSWDRKCKDGLYQALKETHPHLIMEL----WEKGSKK 88
                                                                                                                                                                                                                                   Query Match
14.2%; Score 69.5; DB 2; Length 459;
Best Local Similarity 32.0%; Pred. No. 29;
Matches 16; Conservative 10; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
14.2%; Score 69.5; DB 2; Length 6
Best Local Similarity 30.6%; Pred. No. 41;
Matches 26; Conservative 19; Mismatches 31; Indels
C,Genetics:
A,Gene: GDB:OIAS
A,Cross-references: GDB:119465; OMIM:164350
A,Map position: 12pter-12qter
C,Superfamily: oligo(A) synthetase
C,Keywords: alternative splicing; nucleotidyltransferase
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261 LDAVGVYREELSAIVAPLEASL-KVTEQ-LSSEQSDKIEQHNKXMSQYKE--HITSEFEK 316

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Search completed: July 28, 2004, 08:55:19 Job time: 15.7349 secs

• **x**

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Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

July 28, 2004, 08:51:17; Search time 16.5964 Seconds

(without alignments)
295:514 Million cell updates/sec

Title:

US-09-996-617-2_COPY_1335_1429

Sequence:

1 LHFVDQYREQLIARYTSVEV......HLIMELWEKGSKKGLLPLSS 95

Scoring table: BLOSUM62

Searched:

389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

1 | cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
2 | cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
3 | cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4 | cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
5 | cgn2_6/ptodata/2/iaa/Bep:*
5 | cgn2_6/ptodata/2/iaa/Becyle.
5 | cgn2_6/ptodata/2/iaa/Becyle.
5 | cgn2_6/ptodata/2/iaa/Becyle.
5 | cgn2_6/ptodata/2/iaa/Becyle.
5 | cgn2_6/ptodata/2/iaa/Becyle.
5 | cgn2_6/ptodata/2/iaa/Becyle.
5 | cgn2_6/ptodata/2/iaa/Becyle.
5 | cgn2_6/ptodata/2/iaa/Becyle.
5 | cgn2_6/ptodata/2/iaa/Becyle.
5 | cgn2_6/ptodata/2/iaa/Becyle.
5 | cgn2_6/ptodata/2/iaa/Becyle.
5 | cgn2_6/ptodata/2/iaa/Becyle.
5 | cgn2_6/ptodata/2/iaa/Becyle.
5 | cgn2_6/ptodata/2/iaa/Becyle.
5 | cgn2_6/ptodata/2/iaa/Becyle.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	App1	Appl	Appl	Appl	Appli	Appli	Appl	Appli	Appl	Appli	Appl	Appl:	Appl	Appl	Appl
g !	61,	49,	58,	57,	99	71,	4	4,	4	41,	39,	39,	39,	39,	46,	46,	00	8	43,	ω,	43,		43,	8		47,	
Description	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Seguence	Sequence	Seguence	Sequence	Seguence	Seguence	Seguence	Sequence	Seguence	Seguence	Seguence	Seguence	Seguence	Seguence	Seguence	Seguence
OI	-09-34	-09-340-6	-09-34	-09-340-	-09-340-6	-09-340-	-09-245-2	09-207-	340-620A-	19-865-	19-245-2	-09-207-	6	-09-865-3	-09-207-3	-09-865-36	-660-60-	09-245	245	19-207	39-207-3	-09-340-	-09-34	-09-865-36	-09-865-36	9-207-35	US-09-865-364-47
DB	4	4	4	4	4	4	4	4	4	4	4	44	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4
Length	193	195	71	70	70	109	164	164	164	164	249	249	249	249	409	409	953	953	953	953	953	953	953	953	953	996	996
% Query Match	Н	•	44.1	•	N	22.8		•	•	14.7	٠	14.7	14.7	٠	•	٠	14.7	•	14.7	•	•	٠	14.7	٠	14.7	14.7	14.7
Score	Ŋ	ന	216	0	20	111.5	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72
Result No.	1	7	m	4	Ŋ	9	7	ω	თ	10	11	. 12	13	14	15	16	17	18	61	20	21	22	23	24	25	126	27

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11,	Sequence 11, Appl	11,	Sequence 10, Appl	Sequence 10, Appl	Sequence 10, Appl	Sequence 10, Appl	10,	Sequence 19, Appl	Sequence 19, Appl	Sequence 2, Appli	7	Sequence 12069, A	Sequence 11, Appl		2, 7	Sequence 2, Appli
US-08-436-771-11	US-08-434-998-11 US-08-487-797-11	PCT-US95-02058-11	US-09-039-041A-10	US-09-245-281-10	US-09-207-359B-10	US-09-340-620A-10	US-09-865-364-10	US-08-840-146-19	US-09-360-220-19	US-08-844-086-2	US-09-018-211-2	US-09-489-039A-12069	US-08-973-005A-11	US-09-758-282B-206	US-08-785-428-2	US-08-996-797-2
(7 1°)	<i>1</i> (1)	Ŋ	4	4	4	4	4	m	m	N	ო	4	4,	4	Н	N
400	400	400	100	100	100	100	100	365	365	833	833	341	389	839	804	804
14.6	14.6	14.6	14.5	14.5	14.5	14.5	14.5	14.2	14.2	14.1	14.1	13.8	13.8	13.6	13.5	13.5
71.5	71.5	71.5	71	71	71	71	71	69.5	69.5	69	69	67.5	67.5	66.5	99	99
7 78	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: BERLIA.

APPLICANT: BERLIA.

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERR

FILE REFERENCE: 07334-124001

CURRENT APPLICATION NUMBER: US/09/340,620A

CURRENT FILING DATE: 1999-02-05

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1998-12-08

PRIOR FILING DATE: 1998-02-06

PRIOR FILING DATE: 1998-02-06

PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 71

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
US-09-340-620A-49
US-09-340-620A-49
; Sequence 49, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
    APPLICANT: Bertin, Ohn
    FILE REFERENCE: 07334-124001
; FILE REFERENCE: 07334-124001
; CURRENT FILING DATE: 199-06-28
; CURRENT FILING DATE: 199-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 HFVDQYREQLIARVTSVEVVLDKLHGQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDRK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
51.6%; Score 253; DB 4; Length 193
Best Local Similarity 61.2%; Pred. No. 3.Se-23;
Matches 49; Conservative 11; Mismatches 20; Indels
          Sequence 61, Application US/09340620A Patent No. 6482933 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 CKDGLYQALKETHPHLIMEL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Mus musculus
US-09-340-620A-61
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Sequence 66, Application US/09340620A

Sequence 66, Application US/09340620A

Patent No. 6482933

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE: 07334-124001

CURRENT FILING DATE: 1999-06-28

PRIOR PELLOR TON NUMBER: US 09/245,281

PRIOR PELLOR DATE: 1998-02-05

PRIOR PELLOR DATE: 1998-02-05

PRIOR PELLOR DATE: 1998-02-05

PRIOR PELLOR NUMBER: US 09/099,041

PRIOR PELLOR NUMBER: US 09/099,041

PRIOR PILING DATE: 1998-06-17

PRIOR PELLOR TON NUMBER: US 09/019,942

PRIOR PELLOR PELLOR NUMBER: US 09/019,942

PRIOR PELLOR PELLOR NUMBER: US 09/019,942

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PRIOR PELLOR PELLOR NUMBER: US 09/019,942

PRIOR PELLOR PELLOR NUMBER: US 09/019,942

PRIOR PELLOR 
      TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE FILE REFREENCE: 07334-114001

CURRENT APPLICATION NUMBER: US/09/340,620A

CURRENT APPLICATION NUMBER: US 09/245,281

PRIOR APPLICATION NUMBER: US 09/245,281

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1998-12-08

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 71

SOFFWARE: FEALSEQ FOR Windows Version 4.0

SEQ ID NO 57

LENGTH: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 HFVDQYREQLIARVTSVEVVLDKLHGQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDRK 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 209; DB 4; Length 70
Pred. No. 2.3e-18;
8; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-340-620A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 CKDGLYQAL 70
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; ORGANISM: Mus musculus
US-09-340-620A-66
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Best Local Similarity
Matches 42; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 42; Conserv
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US-09-340-620A-58
i Sequence 58, Application US/09340620A
i Patent No. 6482933
i GENERAL INFORMATION:
APPLICANT BETLIN. John
ITILE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE: 07334-124001
CURRENT APPLICATION NUMBER: US/09/340,620A
CURRENT APPLICATION NUMBER: US 09/245,281
PRIOR PILING DATE: 1999-06-26
PRIOR FILING DATE: 1998-02-05
PRIOR FILING DATE: 1998-02-05
PRIOR FILING DATE: 1998-02-06
PRIOR FILING DATE: 1998-02-06
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 59
LENGTH: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LHFVDQYREQLIARVTSVEVVLDKLHGQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.2%; Score 236; DB 4; Length 195; llarity 56.8%; Pred. No. 4.3e-21; Conservative 17; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 216; DB 4; Length 71;
; Pred. No. 3.2e-19;
12; Mismatches 15; Indels
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION WURBER: US 09/207,359
PRIOR FILING DATE: 1998-12-08
PRIOR PLILING DATE: 1998-12-08
PRIOR PLILING DATE: 1998-06-17
PRIOR PLILING DATE: 1998-06-17
PRIOR PLILING DATE: 1998-06-17
PRIOR PLILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FastSEQ for Windows Version 4.0
SSOTUMARE: PastSEQ for Windows Version 4.0
PRIOR PLILING DATE: 1998
CRGAMISM: Homo sapiens
US-09-340-620A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 TCKDLLLQALRESQSYLVEDL 192
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US-09-340-620A-57
IS-09-340-620A-57
Patent No. 6482933
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 61.4%;
Matches 43; Conservative 13
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Best Local Similarity
Matches 46; Conserv
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GENERAL INVOCATION: John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THER
FILE REPERENCE: 073344-12401
CURRENT APPLICATION NUMBER: US/09/340,620A
CURRENT FILING DATE: 1999-06-28
PRIOR PRILING APPLICATION NUMBER: US 09/245,281
PRIOR PILING DATE: 1998-102-05
PRIOR FILING DATE: 1998-102-08
PRIOR FILING DATE: 1998-104-08
PRIOR FILING DATE: 1998-104-17
PRIOR FILING DATE: 1998-104-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BERLIN, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REPERENCE: 07334-112001
CURRENT TILING DATE: 1998-12-08
PRIOR PILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PRECEDE OF Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46; Indels
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29.7%; Pred. No. 0.42;
ive 14; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                        Sequence 41, Application US/09207359B Patent No. 6469140 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 41, Application US/09340620A
Patent No. 6482933
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Best Local Similarity 29.7%
Matches 27; Conservative
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US-09-207-359B-41
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US-09-340-620A-41
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Best Local Similarity
Matches 27; Conserv
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LENGTH: 164
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APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE: 07334-124001
CURRENT APPLICATION NUMBER: US/09/340,620A
CURRENT APPLICATION NUMBER: US/09/245,281
PRIOR FILING DATE: 1999-06-28
PRIOR PELICATION NUMBER: US 09/207,359
PRIOR PELICATION NUMBER: US 09/207,359
PRIOR PLILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR PLILING DATE: 1998-06-17
PRIOR PLILING DATE: 1998-02-06
NUMBER: US 09/019,942
NUMBER: PRECATION NUMBER: US 09/019,942
NUMBER: PRECATION NUMBER: US 09/019,942
NUMBER: PRECATION NUMBER: US 09/019,942
NUMBER: PRECATION NUMBER: US 09/019,942
NUMBER: PRECATE: 1998-02-06
NUMBER: PRECATE THING DATE: 1998-02-06
NUMBER: PRECATE THING DA
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Sequence 41, Application US/09245281
Sequence 41, Application US/09245281
Setent No. 6369196
GENERAL INFORMATION:
APPLICANT BERTIN, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOUSES THEREOF
FILE REPERENCE: 0734/118001
CURRENT APPLICATION NUMBER: US 09/207,359
EARLIER PLILING DATE: 1999-02-05
EARLIER PLILING DATE: 1999-06-17
EARLIER PLILING DATE: 1999-06-17
EARLIER PLILING DATE: 1999-06-17
EARLIER PLILING DATE: 1999-06-17
EARLIER PLILING DATE: 1999-06-17
EARLIER PLING DATE: 1999-06-17
EARLIER PLING DATE: 1999-06-17
EARLIER PLING DATE: 1999-06-17
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
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Best Local Similarity 42.0%; Pred. No. 3.6e-06;
Matches 34; Conservative 15; Mismatches 25
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Best Local Similarity 29.7%; Pred. No. 0.42;
Matches 27; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1)...(109)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-340-620A-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION: Consensus sequence
                                                   Sequence 71, Application US/09340620A
Patent No. 6482933
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US-09-245-281-41
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APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL WOLESCULES OF THE CARD-RELATED PROTEIN FAMILY
FILE PEPERENCE: 07334/118001
CURRENT TILING DATE: 1999-02-05
FARLIER APPLICATION NUMBER: US 09/207,359
EARLIER APPLICATION NUMBER: US 09/207,359
EARLIER PILING DATE: 1998-12-06
FARLIER APPLICATION NUMBER: US 09/099,041
EARLIER FILING DATE: 1998-06-17
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 39
COFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 39
MANDE. NO 39
MANDE. NO 39
MANDE. NO 39
REQLIARVISVEVVLDK-LHGQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDRKCKD-- 64
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                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFRENCE: 07334-112001
CURRENT PLING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-01-06
SEQ ID NOS: 47
LENGTH: 164
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14.7%; Score 72; DB Best Local Similarity 29.7%; Pred. No. 0.42
Matches 27; Conservative 14; Mismatches
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                                                                                                       65 -GLYQALKETHPHLIMELWEKGSKKGLLPLS
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Patent No. 6613521
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Patent No. 6369196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT; ORGANISM: Homo sapiens US-09-865-364-41
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, ORGANISM: Homo sapiens
US-09-245-281-39
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US-09-245-281-39
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US-US-34U-bZUM-39

Sequence 39, Application US/09340620A

Fatent No. 6482933

GENERAL INFORMATION:
PAPLICANT BERTIN, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE: 07334-124001

CURRENT FILING DATE: 1999-06-28

PRIOR APPLICATION NUMBER: US 09/245,281

PRIOR APPLICATION NUMBER: US 09/207,359

PRIOR APPLICATION NUMBER: US 09/207,359

PRIOR FILING DATE: 1998-12-08

PRIOR PELING DATE: 1998-12-08

PRIOR APPLICATION NUMBER: US 09/099,041

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

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PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-12-08

NUMBER OF SEQ ID NOS: 71

SOFTWARE: PERT PRIOR WINDOWS VERSION 4.0

SEQ ID NO 39

TYPE: PRI

TYPE: PRI

TYPE: PRI

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                                                                                             4; Gaps
Query Match
14.7%; Score 72; DB 4; Length 249;
Best Local Similarity 29.7%; Pred. No. 0.72;
Matches 27; Conservative 14; Mismatches 46; Indels
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14.7%; Score 72; DB 4; Length 249;
Best Local Similarity 29.7%; Pred. No. 0.72;
Matches 27; Conservative 14; Mismatches 46; Indels
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APPLICANT: Bertin, John
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
TITLE OF INVENTION: PROTEIN 12001
CURRENT FAPLICATION NUMBER: US/09/207,359B
CURRENT FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 4.0
SERGIH: 249
TYPE: PRI
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VS-09-2070 359B-39
Sequence 39, Application US/09207359B
Patent No. 6469140
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US-09-207-359B-39
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US-09-340-620A-39
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ORGANISM: Artificial Sequence
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                                                         DB 4; Length 249;
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Fatent No. 6613521
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL WOOF 09/09/0665,364
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 39
INSTEMBLE 1249
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GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 07334-112001
CURRENT FILING DATE: 1998-12-08
CURRENT FILING DATE: 1998-12-08
FRICK FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
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Best Local Similarity 29.7%; Pred. No. 0.72;
Matches 27; Conservative 14; Mismatches
                                                         Query Match 14.7%; Score 72; DB 4; Best Local Similarity 29.7%; Pred. No. 0.72; Matches 27; Conservative 14; Mismatches
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, ORGANISM: Homo sapiens
US-09-865-364-39
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        US-09-340-620A-39
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Sequence 3, Appli
Sequence 26, Appl
Sequence 11, Appl
Sequence 3, Appli
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Sequence 2, Appli
Sequence 8, Appli
Sequence 15, Appl
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Sequence 2, Appli
Sequence 2, Appli
                                                                                                      July 28, 2004, 08:54:53; Search time 46.3554 Seconds (without alignments) 642.856 Million cell updates/sec
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Sequence 3, A
Sequence 15,
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1: \cgn2_6/ptodata/1/pubpaa/PCT_RBW PUB.Pep:*
2: \cgn2_6/ptodata/1/pubpaa/PCT_RBW PUB.Pep:*
3: \cgn2_6/ptodata/1/pubpaa/PCT_RBW PUB.Pep:*
4: \cgn2_6/ptodata/1/pubpaa/USO6_NBW PUB.Pep:*
5: \cgn2_6/ptodata/1/pubpaa/USO6_NBW PUB.Pep:*
5: \cgn2_6/ptodata/1/pubpaa/USO7_NBW PUB.Pep:*
7: \cgn2_6/ptodata/1/pubpaa/USO8_NBW_PUB.Pep:*
7: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.Pep:*
8: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.Pep:*
9: \cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.Pep:*
11: \cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.Pep:*
12: \cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.Pep:*
13: \cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.Pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-996-617-2

US-09-31-071-2

US-10-029-347-3

2. US-10-029-347-26

4. US-10-028-374-3

4. US-10-028-374-3

4. US-10-028-374-3

4. US-10-183-770-3

4. US-10-183-770-15

US-09-388-221-2

US-09-388-221-2

US-10-183-770-15

US-09-184-315-15
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490
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                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Sequence 139, App	Sequence 7, Appli	a	6	ď	•	•••	œ	Sequence 8, Appli	<u>_</u>	4	ထ	'n	0)	a)	a)	ω	Sequence 5, Appli	5421	4	15,	e 15	28,	e 58	57,		e 57	Sequence 66, Appl	7	54
10 US-09-895-298-139	9 US-09-841-879B-7	16 US-10-756-097-7	US-09-728-721-	US-09-841	US-10-295-9	6 US-10-756~	9 US-09-841-879B-8	6 US-10-756	9 US-09-931-071-7	US-09-728-	6-60-SD	US-09-8	US-10-44	US-10-295-981-4	Ŋ	5 US-10-131-410-	US-10-75	US-10	US-09-895-298-1	9 US-09-841-879B-15	6 US-10-756-097-1	US-09-728-721-5	4 US-1	0S-09	9 US-09-728-721-66	4 US-10-295-981-5	4 US-10-29	10 US-09-895-298-146	US-10-10
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ALIGNMENTS

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US-09-388-221-4

Sequence 4, Application US/09388221A

Sequence 4, Application US/09388221A

Publication No. US2020192643A1

GENERAL INFORMATION:

APPLICANT: Reed, John C.

TITLE OF INVENTION: No. US20020192643A1e1 Card Proteins Involved in Cell Death Regul

FILE REFERENCE: P-1J 3650

CURRENT APPLICATION UNMBER: US/09/388,221A

CURRENT FILING DATE: 1999-09-01

NUMBER OF SEQ ID NOS: 18
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US-09-96-617-2
Second 2. Application US/09996617
Fatent No. US20020128198A1
GENERAL INFORMATION:
APPLICANT: BELTIN, John
TITLE OF INVENTION:
TITLE OF INVENTION:
NOVEL MOLECULES OF THE CARD-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1365 KCKDGLYQALKETHPHLIMELWEKGSKKGLLPLSS 1399
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100.0%; Pred. No. 7.3e-46;
rative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                           LENGTH: 1399
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SEQ ID NO 4
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Pedication No. US20030017562A1
GENERAL INFORMATION:
APPLICANT: Bristol-Wyers Squibb Company
TITLE OF INVENTION: A NOVEL HUMAN LEUCINB-RICH REPEAT CONTAINING PROTEIN EXPRESSED
TITLE OF INVENTION: PREDOMINATELY IN SMALL INTESTINE, HLRRSI1
CURRENT APPLICATION NUMBER: US/10/029,347
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
SEQ ID NO 26
LENGTH: 1429
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Publication No. US20030087340A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PREDOMINATELY IN NERVOUS SYSTEM TISSUES, HLRRNS1
TITLE OF INVENTION: PREDOMINATELY IN NERVOUS SYSTEM TISSUES, HLRRNS1
FILE REPERENCE: D00085.np
CURRENT APPLICATION NUMBER: US/10/028,392
CURRENT APPLICATION NUMBER: US 60/259,479
PRIOR FILING DATE: 2001-01-03
PRIOR FILING DATE: 2001-01-03
PRIOR FILING DATE: 2001-01-03
PRIOR FILING DATE: 2001-01-03
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 63
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        PREDOMINATELY IN SMALL INTESTINE, HLRRSI1
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TITLE OF INVENTION: PREDOMINATELY IN SMAL
FILE REFERENCE: D0066
CURRENT APPLICATION NUMBER: US/10/029,347
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT; ORGANISM: homo sapiens US-10-029-347-26
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ORGANISM: homo sapiens
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US-10-028-392-11
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US-10-029-347-26
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Best Local S:
Matches 95
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; Sequence 3, Application US/10029347
; Publication No. US20030017562A1
; Publication INFORMATION:
; AFPLICANT: Bristol Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN EXPRESSED
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APPLICANT: Bertin, John
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
TITLE REFERENCE: 07334-33501
CURRENT APPLICATION NUMBER: US/09/931,071
CURRENT APPLICATION NUMBER: 09/428,252
PRIOR APPLICATION NUMBER: 09/428,252
PRIOR APPLICATION NUMBER: 09/428,252
PRIOR PRING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
     TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF FILE REFERENCE: 07334-340001
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100.0%; Pred. No. 7.5e-46;
ive 0; Mismatches 0;
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                                                FILE REFERENCE: 0.53 = 340.09, 996,617
CURRENT APPLICATION NUMBER: US/09/996,617
CURRENT FILING DATE: 2001-11-27
PRIOR PELING DATE: 2001-08-15
PRIOR FILING DATE: 1999-10-27
PRIOR RIGHT DATE: 1999-10-27
PRIOR PLING DATE: 1999-06-28
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 2
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Patent No. US20020128219A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 95; Conservative
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CORGANISM: Homo sapiens
US-09-996-617-2
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; ORGANISM: Homo sapiens
US-09-931-071-2
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US-09-931-071-2
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US-10-183-770-3

Sequence 3, Application US/10183770

Fublication No. US2033180812A1

Sequence 3, Application US/10183770

Fublication No. US2033180812A1

FUBLICANT: Bristol-Myers Squibb Company

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: A NOVEL HUMAN LEGCINE-RICH REPEAT CONTAINING PROTEIN EXPRESSED

TITLE OF INVENTION: PREDOMINATELY IN BONE MARROW, HLRREM1

FILE REFERENCE: D0067A CIP

CURRENT APPLICATION NUMBER: US/10/183,770

PRIOR APPLICATION NUMBER: US 60/257,773

PRIOR APPLICATION NUMBER: US 10/028,374

PRIOR FILING DATE: 2000-12-20

NUMBER OF SEQ ID NOS: 33

SOFURMARE: PatentIn Version 3.1

FEMALICATION NOS: 33

SEQ ID NO 3

FEMALICATION NOS: 33

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VERNERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN EXPRESSED

TITLE OF INVENTION: REDOMINATELY IN BONE MARROW, HLRREMI

FILE REFERENCE: D0067A CIP

CURRENT APPLICATION NUMBER: US/10/183,770

CURRENT FILING DATE: 2000-06-27

PRIOR APPLICATION NUMBER: US 10/028,374

PRIOR PRIOR DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin version 3.1

SEQ ID NO 15

LENGTH: 1429

TYPE: PRT

CREATING DATE: D001-15

TYPE: PRT

CREATING DATE: 2001-12-10

NUMBER: PATENTIAL NOS: 33

CONTAINED: PRESENTED:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1335 LHFVDQYREQLIARVISVEVVLDKLHGQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDR 1394
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                                                              Length 1429;
                                                                                                                                       Indels
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                                                              Query Match
100.0%; Score 490; DB 14;
Best Local Similarity 100.0%; Pred. No. 7.5e-46;
Matches 95; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 95; Conservative
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US-10-183-770-3
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US-10-028-374-15
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Publication No. US20030143706A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BAISTO-HONE
TITLE OF INVENTION:
PRICE PREPERT CONTAINING PROTEIN EXPRESSED
TITLE OF INVENTION:
PRICE PREPERT APPLICATION NUMBER: US/10/028,374

CURRENT APPLICATION NUMBER: US 60/257,773

PRIOR PRILING DATE: 2000-12-22

NUMBER OF SEQ ID NOS: 22-22

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US-10-028-374-15

Sequence 15, Application US/10028374

Publication No. US20030143706A1

Sequence 15, Application US/10028374

Publication No. US20030143706A1

APPLICATION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN EXPRESSED

TITLE OF INVENTION: PREDOMINATELY IN BONE MARROW, HIRREM1

FILE REFERENCE: D0067NP

CURRENT APPLICATION NUMBER: US/10/028,374

CURRENT FILING DATE: 2001-12-20

PRIOR APPLICATION NUMBER: US 60/257,773

PRIOR APPLICATION NUMBER: US 60/257,773

PRIOR FILING DATE: 2000-12-22

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin version 3.0
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Best Local Similarity 100.0%; Pred. No. 7.5e-46;
Matches 95; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                           Length 1429;
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100.0%; Score 490; DB 14;
Best Local Similarity 100.0%; Pred. No. 7.5e-46;
Matches 95; Conservative 0; Mismatches 0;
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SOFTWARE: PatentIn version 3.0 SEQ ID NO 11 LENGTH: 1429 TYPE: PRI
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LENGTH: 1429
TYPE: PRT
ORGANISM: homo sapiens
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CRGANISM: homo sapiens
US-10-028-374-3
                                                                                                                                       ; ORGANISM: homo sapiens
US-10-028-392-11
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Squence 15, Application US/09841739

Squence 15, Application US/09841739

Patent No. US2002034784A1

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
TITLE OF INVENTION: NOVEL WOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
OURRENT FILING DATE: 2001-08-29

PRIOR FILING DATE: 2001-10-29

PRIOR FILING DATE: 2001-10-27

PRIOR FILING DATE: 2001-10-27

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NOS: 16
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                                                                                                            Sequence 8, Application US/10182822A, Sequence 8, Application US/1018282A, Publication No. US20030211493A1
GENERAL INFORMATION:
APPLICANT: NOVTE GENONICS, INC.; BAUGHN, Mariah R. APPLICANT: NOVTE GENONICS, INC.; BAUGHN, Mariah R. TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS; FILE REFERENCE: PI-0032 USN
CURRENT APPLICATION NUMBER: US/10/182,822A, CURRENT FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: US 60/180,093
PRIOR FILING DATE: 2000-02-02
PRIOR FILING DATE: 2000-02-02
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL PROGRAM
SEQ ID NOS: 42
LENGTH: 1473
1439 KCKDGLYQALKETHPHLIMELWEKGSKKGLLPLSS 1473
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Best Local Similarity 100.0%; Pred. No. 2.8e-40;
Matches 82; Conservative 0; Mismatches 0;
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NAME/KEY: misc feature OTHER INFORMATION: 1ncyte ID No: 4250893CD1
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ORGANISM: Homo sapiens
US-09-841-739-15
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US-09-841-739-15
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TITLE OF INVENTION: No. US20020192643Alel Card Proteins Involved in Cell Death Regul
FILE REFERENCE: P-LJ 3650
CURRENT APPLICATION UNDER: US/09/388,221A
CURRENT FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
TENGTH: 1443
TENGTH: 1443
TAPE: PRT
CURRENT: TAPE: PRT
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COGANISM: Homo sapiens
US-09-388-221-6
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TITLE OF INVENTION: No. US20020192643Alel Card Proteins Involved in Cell Death Regul
TITLE REPERENCE: P-LJ 3650
CURRENT APPLICATION NUMBER: US/09/388,221A
CURRENT FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIN Ver. 2.1
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                       Query Match 100.0%; Score 490; DB 14; Best Local Similarity 100.0%; Pred. No. 7.5e-46; Matches 95; Conservative 0; Mismatches 0;
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Pred. No. 7.6e-46;
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100.0%; Score 490; DB 9;
Best Local Similarity 100.0%; Pred. No. 7.8e-46;
Matches 95; Conservative 0; Mismatches 0;
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SEQ ID NO 2
LENGTH: 1473
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US-09-388-221-6
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US-09-388-221-2
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RESULT 15

US-10-449-315-15

Sequence 15, Application US/10449315

Publication No. US2030190679A1

GENERAL INFORMATION:

APPLICANT: Betrin. John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE: 07334-329001

CURRENT APPLICATION NUMBER: US/10/449,315

PRIOR APPLICATION NUMBER: US /09/641,739

PRIOR FILING DATE: 2001-08-29

PRIOR FILING DATE: 2001-08-29

PRIOR FILING DATE: 1999-10-27

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 15

LENGTH: 88

TTYPE: PRI
TTYPE: PRI
ORGANISM: Homo sapiens

US-10-449-315-15
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87.1%; Score 427; DB 14; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.8e-40;
Matches 82; Conservative 0; Mismatches 0; Indels
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61 KCKDGLYQALKETHPHLIMELW 82
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AAY72670 standard; protein; 1397 AA.
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GenCore version 5.1.6
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ALIGNMENTS

1. .956 /note= "Corresponds to 1-956 residues of human NAC beta isoform (AAY72669)" 957. .1229 /note= "Corresponds to 988-1260 residues of human NAC beta isoform (AAY72669)" 1230. .1397 /note= "Corresponds to 1306-1473 residues of human NAC beta isoform (AAY72669)" Novel nucleic acid encoding NB-ARC and caspase associated recruitment domains, used to produce polypeptides for screening for modulators of apoptosis. Human, NB domain; nucleotide binding domain; NB-ARC and CARD; NAC; caspase-associated recruitment domain; CARD; TIM-Barrel-like domain; cystelaine appartyl protease; apoptosis; cytokine production; cytokine receptor signalling; therapy; inflammatory disorder; sepsis; fibrosis; arthritis; cancer; adenocarcinoma; leukaemia. Human NB-ARC and CARD containing protein (NAC) gamma isoform. Location/Qualifiers 99US-00388221. 01-SEP-2000; 2000WO-US024152. (BURN-) BURNHAM INST. WPI; 2001-183258/18. N-PSDB; AAD02761. WO200116170-A2 Homo sapiens. 01-SEP-1999; 08-MAR-2001. Reed JC; Key Region Region Region

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27-OCT-2000; 2000WO-US029796.
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                                                                  The present sequence is a human NB-ARC and CARD containing protein (NAC) gamma isoform. Nac gamma isoform represents the NAC splice variant in which both the splice regions are absent in the translated polypeptide. NAC protein comprises a nucleotide binding (NB) domain (also referred as NB-ARC domain). A caspasse-associated recruitment domain (CARD) and a TIM-BARC domain. The caspasse; cysteine aspartyl protease, are principal effectors of apoptosis. CARD containing NAC proteins are used for screening modulates spoptosis, cytokine production, cytokine receptor signalling and other cellular processes. NAC can an immunogen for the production of polyclonal and monoclonal antibodies. It can also be used to diagnose and treat inflammatory disorders such as sepsis, fibrosis and arthritis and cancer pathologies such as adenocarcinomas and leukaemias
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950. .976
/note= "leucine-rich domain"
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/note= "kinase 2 subdomain"
454. .463
Claim 15; Page 143-148; 184pp; English.
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The invention relates to identifying compounds, that modulate interaction between caspase recruitment domain (CARD)-7 and CARD-5. The method involves measuring the binding of CARD-7 and CARD-5 in the presence of the compound (an increase in the binding of CARD-7 to CARD-5 in the presence of the compound compared to the binding in the absence of the compound indicates that the compound is a modulator of CARD-7-CARD-5 in the presence of the compound indicates that the compound is a modulator of CARD-7-CARD-5 in the presence of the compound indicates that the compound is a modulator of CARD-7 and CARD-8 expression or activity can be used to treat or diagnose disorders such as cancers, bacterial or viral infections, untoinmuned disorders (systemic lupus erythematosus, immune-mediated glomerulonephritis or arthritis) inflammatory disorders, organ-specific autoimmunity including multiple sclerosis, Hashimoto's thyroiditis, or Grave's disease, psoriasis, graft rejection, allergies. CARD-7 and CARD-8 are useful as modulating agents in regulating a variety of cellular processes including cell growth and cell death. The present sequence represents the human CARD-7, an intracellular protein
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or

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The invention relates to isolated nucleic acid molecules (I) encoding human leucine-rich repeat small intestine I (HLRRSII) polypeptides. The nucleic acid molecules and polypeptides are useful for preventing, conditions, such as proliferative, creating and ameliorating medical conditions, such as proliferative, creating and ameliorating medical conditions, such as proliferative, condition, either directly or indirectly. They are also useful for treating, preventing and/or diagnosing diseases, disorders and/or conditions of: immune system conditions or inhibiting the proliferation, differentiation, or mobilisation of immune cells, haematopoietic cells e.g. thrombocytopenia, anaemia; immunologic deficiency syndromes, e.g. human immune deficiency virus (HVV) infection, HTLV-BLV infection; blood coagulation disorders, e.g. atterial thrombosis; autoimmune disorders, e.g. Addison's disease, c.g. chronic prostatitis, sepsis; proliferative disorders, e.g. cancer; cardiovascular disorders, e.g. arrhythmia, mycocadial ischaemias, aneurological disorders, e.g. measles, mumps, pneumonia, or viral, cardiovascular differences, e.g. measles, mumps, pneumonia, or viral, concea; infectious diseases, e.g. measles, mumps, pneumonia, or viral, concea; infectious diseases, e.g. measles, mumps, pneumonia, or viral, concea; and fungal infections. The HRRSII polypeptides are useful for modulating cytokine production, antigen presentation, or other processes such as boosting immune responses. HBG78454-ABG78474 represent HIRRSII camino acid sequences and related amino acid sequences of the invention
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                                                                                                                                                                                                                                                                           New isolated nucleic acid molecules encoding HLRRSIl polypeptides, or their fragments and homologues, useful for preventing, treating and ameliorating medical conditions, e.g. proliferative, gastrointestinal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 2; 336pp; English.
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                                                                                                      22-DEC-2000; 2000US-0257774P.
                                                              20-DEC-2001; 2001WO-US049739
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                                                                                                                                                  (BRIM ) BRISTOL-MYERS
                                                                                                                                                                                                                                        WPI; 2002-619252/66.
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Best Local Similarity
Matches 95; Conserv
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                  08-AUG-2002,
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the invention relates to isolated nucleic acid molecules (I) encoding the invention relates to isolated nucleic acid molecules and polypeptides are useful for preventing.

Comucleic acid molecules and polypeptides are useful for preventing, contacting medical conditions, such as proliferative, gastrointestinal, renal, neural, or reproductive disorders; or disorders related to aberrant calcium regulation or apoptorsis modulation, either directly or indirectly. They are also useful for treating, preventing and/or diagnosing diseases, disorders and/or conditions of: immune system conditions of immune cells; haematopoietic cells e.g. thrombocytopenia, anaemia; immunologic deficiency syndromes, e.g. human immune deficiency virus (HIV) infection, HTLV-BLV infection; blood coaqulation disorders, c.g. arterial thrombosis; autoximune disorders, e.g. Addison's disease, c.g. chronic prostatiis, sepsis; proliferative disorders, e.g. cancer; cardiovascular disorders, e.g. arrhythmia, myocardial ischaemias, corrected risorders, e.g. arrhythmia, myocardial ischaemias, corrected risorders, e.g. arrhythmia, myocardial ischaemias, chorea; infectious diseases, e.g. Alzheimer's disease, Huntington's chorea; infectious diseases, e.g. Alzheimer's disease, Huntington's concertial, and fungal infections. The HIRSII polypeptides are useful for modulating cytokine production, anigen presentation, or other processes cuch as boosting immune responses. ABG78454-ABG78474 represent HIRRSII omino acid sequences and related amino acid sequences of the invention
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inflammatory condition; cardiovascular disorder; ischaemia; neurological disorder; infectious disease; cytokine production; expressed sequence tag; EST.
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Pred. No. 2.2e-48;
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es 95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       renal disorders.
                                                                                                                               WO200261086-A2.
                                                                                       Unidentified
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Leucine rich repeat; nervous system; human; neural disorder; apoptosis; renal disorder; immune disorder; arthritis; asthma; AIDS; acquired immunodeficiency syndrome; rheumatoid arthritis; haematopoietic disorder; metabolic disorder; reproductive disorder; pulmonary disease; cardiovascular disease; hyperproliferative disorder; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; haemolytic anaemia; autoimmune disease; allergic encephalomyelitis; gene therapy.

WO200274959-A2.

Homo sapiens.

Human leucine rich repeat domain containing protein #2

(first entry)

07-JAN-2003

ABG97969;

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ABG97969 standard; protein; 1429

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The present sequence represents a human leucine-rich repeat domain containing protein, which was used as a probe to search for leucine-rich repeat containing protein HIRRBMI Polypeptides and pelpatides and polymerleotides are useful for preventing, treating or ameliorating a disorder related to aberiant apoptosis modulation, either directly or indirectly, and in modulating signal transduction activity in various colls, tissue and organisms. They are also useful for treating, preventing, or diagnosing diseases, allergic conditions (e.g. asthma), cardiovascular disorders, and neurological diseases, and for increasing the organisms ability to synthesize add/or release pheromones. The polypeptide may also be used in treating, preventing or ameliorating pulmonary disease (e.g. chronic obstructive pulmonary disease, allergic rhinitis, on bronchial hyperresponsiveness), reproductive disease, haematopoletic disease, platelet disorders (e.g. innate immunity to bacterial synthogens, or adaptive immune responss, immune and inflammatory diseases and cancers. HirRBMI nucleic acids may further be used in chromosome and cancers. HirRBMI nucleic acids may further be used in chromosome and cancers. HirRBMI nucleic acids may further be used in chromosome and marker, as diagnostic probes, in gene therapy, in raising anti-DNA antibodies, or as antigens for eliciting immune responses
                                        Human; leucine-rich repeat; HLRRBM1; proliferative disorder; immune condition; apoptosis; signal transduction; autoimmune disease; haemeropoietic cell disease; graft-versus-host disease; allergy; asthma; cardiovascular disorder; neurological disease; pheromone; pulmonary disease; chronic obstructive pulmonary disease; allergy; asthma allergic rhinitis; bronchial hyperresponsiveness; reproductive disease; haemeropoietic disease; platelet disorder; Bernard-Soulier syndrome; inflammatory disorder; systemic lupus erythematosus; cardiovascular disease; cancer; KIAA0926.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New HLRRBM1 nucleic acids for preventing, treating or ameliorating e.g. proliferative disorders, immune conditions, a disorder related to aberrant apoptosis modulation or developmental disorders.
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  Human leucine-rich repeat domain containing protein KIAA0926.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mintier G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BRIM ) BRISTOL-MYERS SQUIBB CO.
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Best Local Similarity
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                                                                                                                                                                                                                                                                          Homo sapiens.
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containing proteins expressed in nervous system tissues, HIRRNSI. The HIRRNSI polypeptide or the polymuclectide is useful for preventing, treating proteins expressed in neural disorder or a disorder related to aberrant apoptosis modulation (either directly or indirectly, renal disorder, immune disorder (e.g. arthritis, asthma, acquired inmune disorder (e.g. arthritis, asthma, acquired immune disorder (e.g. arthritis, userna, acquired immunedisorder), reproductive, pulmonary or cardiovascular diseases, hyperproliferative disorders, neurodegenerative diseases (e.g. Alzheimer's disease, parkinson's disease or Huntington's diseases (e.g. Alzheimer's disease, and autoimmune diseases, nervous system diseases and/or disorders, and autoimmune diseases (e.g. Addison's disease, haemolytic anaemia, antiphospholipid syndrome, or allergic encephalomyelitis). The polymucleotides are also useful as chromosome markers, for chromosome identification, gene therapy, and in identifying or aleucine-rich repeat containing protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New HLRRNS1 nucleic acids and polypeptides, useful for preventing, treating, or ameliorating e.g. renal disorder, immune, hematopoietic, metabolic, reproductive, pulmonary, cardiovascular or autoimmune
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100.0%; Pred. No. 2.2e-48;
ive 0; Mismatches 0;
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2001US-0260616P.
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09-JAN-2001;
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Matches 95,
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61 KCKDGLYQALKETHPHLIMELWEKGSKKGLLPLSS 95

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Gaps ö

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LHFVDQYREQLIARVISVEVVLDKIHGQVLSQEQYERVLAENTRPSQWRKIFSLSQSWDR 1394

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KCKDGLYQALKETHPHLIMELWEKGSKKGLLPLSS 95

1 LHFVDQYREQLIARVISVEVVLDKLHGQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDR

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The present invention relates the DNA and their encoded proteins, where the proteins contain at least one PYD (pyrin) domain. These can be used to treat diseases causedated with impaired intracellular signal transduction, particularly inflammation such as psoriasis, arteriosclerosis, bacterial or viral infections (particularly meningitis and pneumonia), multiple sclerosis, rheumatoid arthritis, asthma, sarcoidosis, glomerulonephritis and osteoarthritis, and also Alzheimer's and parkinson's diseases. The present sequence is a protein of the New DNA encoding protein with pyrin domain, useful for treating diseases involving impaired signal transduction, particularly inflammation, also proteins and antibodies. Pyrin domain; PVD domain; antiinflammatory; antiparkinsonian; antiarteriosclerotic; antipsoriatic; antibacterial; virucide; neuroprotective; antiarthritic; antirheumatic; antiasthmatic; nephrotropic; osteopathnic; nootropic; intracellular signal transduction; inflammation; Alzheimer's disease; infection; psoriasis; asthma; arteriosclerosis; multiple sclerosis; rheumatoid arthritis; sarcoidosis; osteoarthritis; glomerulonephritis. 1429 1395 KCKDGLYQALKETHPHLIMELWEKGSKKGLLPLSS Pyrin domain containing protein NALP1-hs. AAO17855 standard; protein; 1429 AA Claim 5; Fig 1; 116pp; German. (APOT-) APOTECH RES & DEV LTD. 15-NOV-2000; 2000DE-01056687. 30-NOV-2000; 2000DE-01059595. 30-OCT-2001; 2001WO-EP012545. (first entry) Martinon WPI; 2002-427093/45. N-PSDB; AAL47127. Sequence 1429 AA; MO200240668-A2. Unidentified 20-AUG-2002 ٦, 23-MAY-2002 AA017855; Tschopp

Gaps .. 0 / Match 100.0%; Score 490; DB 5; Length 1429; Local Similarity 100.0%; Pred. No. 2.2e-48; tes 95; Conservative 0; Mismatches 0; Indels 0; Query Match Best Loca Matches

1335 LHFVDQYREQLIARVISVEVVLDKLHGQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDR 1394 1 LHFVDQYREQLIARVISVEVVLDKLHGQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDR

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1395 KCKDGLYQALKETHPHLIMELWEKGSKKGLLPLSS 1429

KCKDGLYQALKETHPHLIMELWEKGSKKGLLPLSS

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RESULT 8 ABG71631

Human caspase recruitment domain-7 (CARD-7). Ä standard; protein; 1429 09-JAN-2003 (first entry) ABG71631; ABG71631

Human; caspase activity; caspase recruitment domain-7; CARD-7; caspase-1; pseudo-interleukin-1 beta converting enzyme; IL-1beta; pseudoICE; ICEBERG; cell growth, cell death; inflammation; apoptosis; caspase activation; cancer; follicular lymphoma; leukaemia; melanoma; colon cancer; lung carcinoma; viral infection; autoimmune disease; systemic lupus erythematosus; reactive arthritis; systemic lupus erythematosus; reactive arthritis; ALS; Alzheimer's disease; Parkinson's disease; amylorrophic laceral sclerosis; myocardial infarction; stroke; inflammatory disorder; Crohn's disease; minsulin dependent diabetes mellitus; multiple sclerosis; psoriasis; graft rejection; allergic rhinhitis; food allergy; conjunctivitis; glomerular nephritis; cytostatic; virucide; immunosuppressive; dermatological; nephrotropic; neuroprotective; cardiant.

Homo sapiens

US2002128219-A1.

12-SEP-2002.

15-AUG-2001; 2001US-00931071.

99US-00428252. 27-OCT-1999;

(BERT/) BERTIN J. (ALNE) ALNEMRI E S.

Bertin J, Alnemri ES;

WPI; 2003-028968/02. N-PSDB; ABS55497.

Assays for identifying compound that modulates the interaction of caspase recruitment domain-8 with a CARD-8 ligand or a compound that modulates activity of CARD-8. recruitment activity of

Disclosure, Fig 1; 49pp; English.

The present invention relates to methods of identifying compounds that regulate caspase activity using caspase recruitment domain=9 (CARD-8) or caspase recruitment domain=9 (CARD-8). In particular, a method for identifying a compound that modulates the interaction between CARD-8 and caspase-1, pseudo-interleukin-1 (IL-1) beta converting enzyme (pseudoICE) cor ICEBERG is disclosed. CARD-7 and CARD-8 molecules are useful as modulating agents in regulating a variety of cellular processes including cell growth, cell death, and inflammation. The methods of the invention cor increase/decrease apoptosis, or compounds that have the ability to induce caspase increase/decrease apoptosis, or comprise the ability to induce caspase correctly or increase/decrease apoptosis, or comprise the ability to induce caspase activation. The methods are useful for treating disorders associated with an undesirably low rate correctly or treating disorders associated with an undesirably low rate correctly interaction, acloon cancer, lung carcinoma, etc), viral infections, autoimmune diseases caused by low levels of apoptosis (c.g. systemic lupus erythematosus, immune-mediated glomerulonephritis, and arthritis). The methods are also useful for treating disorders with cundesirably high rates of apoptosis such as human immunodeficiency virus (HIV) infection, Alzheimer's disease, spinal muscular atrophy, various forms of cerebellar degeneration, anemia associated with chronic disease, aplastic annemia, chronic neutropaenia, myelodysplastic confusoriates (LIS), retinitis pigmentosas, spinal muscular atrophy, confusores (e.g. crohn's disease, reactive, and various inflammatory confusores (e.g. crohn's disease, reactive, arthritis, insulin dependent diabetes mellitus, multiple sclerosis, psoriasis, graft rejection, allergic rhinitis, food allergies, conjunctiis, graft rejection,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytostatic; nootropic; neuroprotective; antiinflammatory; antisense therapy; NAC; DEFCAP; hyperproliferative disease; apoptosis; death effector filament-forming CED4-like apoptosis protein; neurological disease; infection; inflammation; tumour formation; caspase recruitment domain protein 7.
                                                                                                                                              1 LHFVDQYREQLIARVISVEVVLDXLHGQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDR
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                                                                                                             Gaps
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                                                                           Length 1429;
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 etc). The present sequence represents human CARD-7
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                                                                         Score 490; DB 6;
Pred. No. 2.2e-48;
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                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                               ABP96889 standard; protein; 1429 AA.
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100.0%;
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                                                                                      Similarity 100.
95; Conservative
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                                                                     Query Match
Best Local S
Matches 95
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and prophylaxis, e.g. to prevent or delay infection, inflammation or tumour formation. NAC is also known as a death effector filament-forming CED4-like apoptosis protein (DEFCAP). NAC is located on human chromosome 17p13. The present sequence represents a human caspase recruitment domain protein 7, which is used in an example from the invention
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Pred. No. 2.2e-48;
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                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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and for treating a disease or condition associated with expression of NAC, e.g. hyperproliferative disease, neurological disease, or a disease us diseased ar disease ard disease. The compounds are also useful as research reagents and kits, or for diagnostics, therapeutics and prophylaxis, e.g. to prevent or delay infection, inflammation or tumour formation. NAC is also known as a death effector filament-forming CED4-like apoptosis protein (DEFCAP). NAC is located on human chromosome 17p13. The present sequence represents human NAC, which is used in an example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; caspase activity; caspase recruitment domain-7; CARD-7; caspase-pseudo-interleukin-1 beta converting enzyme; IL-1beta; pseudo-ICE; caspase-greate; call growth, call death; inflammation; apoptosis; caspase activation; cancer; follicular lymphoma; leukaemia; melanoma; colon cancer; lung carcinoma; viral infection; autoimmune disease; systemic lupus erythematosus; reactive arthritis; human immunodeficiency virus infection; HIV infection; ALS; human immunodeficiency virus infection; stockinon; alsease; myocardial infarction; stocke; inflammatory disorder; Crohn's disease; insulin dependent diabetes mellitus; multiple sclerosis; psoriasis; graft rejection; altery, chillis; cytostatic; virucide; immunosuppressive; dermatological; nephrotropic; neuroprotective; cardiant.
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100.0%; Pred. No. 2.2e-48;
ative 0; Mismatches 0;
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27-OCT-1999; 99US-00428252.
15-AUG-2001; 2001US-00931071.
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es 95; Conserv
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                                                                                                                                                                       Sequence 1429 AA;
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Identifying modulator of CARD-7 and CARD-5 interaction, by contacting CARD-7 and CARD-5 in presence of test compound, measuring their binding, and identifying modulator, when binding of CARD-7 to CARD-5 is altered.

Disclosure; Fig 1; 43pp; English

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The present invention relates to methods of identifying compounds that regulate caspase activity using caspase recruitment domain=7 (CARD-7) or caspase recruitment domain=8 (CARD-8). In particular, a method for identifying a compound that modulates the interaction between CARD-8 and caspase-1, pseudo-interleukin-1 (IL-1) beta converting enzyme (pseudoICE) cor ICEBERG is disclosed. CARD-7 and CARD-8 molecules are useful as modulating agents in regulating a variety of Cellular processes including cell growth, cell death, and inflammation. The methods of the invention increase/decrease apoptosis, or compounds that have the ability to induce caspase contration. The methods is increased activation. The methods is not mappropriate inflammation. The methods are useful for treating disorders associated with an undesirably low rate contration. The methods is an electrical associated with an undesirably low rate of apoptosis such as cancer (preferably follicular lymphoma, chronic of apoptosis such as cancer (preferably follicular lymphoma, chronic conference inflammation. The methods are also useful for treating disorders with an undesirably high rates of apoptosis such as immune mediated glomerulonephritis, and arthritis). The methods are also useful for treating disorders with cundesirably high rates of apoptosis such as human immunodeficiency virus (HIV) infection, Alzheimer's disease, spinal muscular atrophy. The conference for syndromes, myocardial infarction, atroke, and various inflammatory disease, aplastic anaemia, chronic neutropaenia, myolodysplastic cylebrates mellitus, multiple solerosis, postables, insular nephritis, allergic rhinitis, food allergies, conjunctivitis, glomerular nephritis, cetc). The present sequence represents human CARD-7
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957. 1442
/note="Corresponds to 988-1473 residues of human NAC beta isoform (AAY72669)"
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100.0%; Pred. No. 2.2e-48;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                              The present sequence is a human NB-ARC and CARD containing protein (NAC) delta isoform. NAC delta isoform represents the NAC splice variant in which one of the splice region is absent in the translated polypeptide. NAC protein comprises a nucleotide binding (NB) domain (also referred as NB-ARC domain), a caspase-associated recruitment domain (CARD) and a TIM-PARC domain). The caspases, cysteine aspartyl proteases, are Brincipal effectors of apoptosis. CARD connealing NAC proteins are used for screening modulators that modulates apoptosis, cytokine production, cytokine receptor signalling and other cellular processes. NAC can act as an immunogen for the production of polyclonal and monoclonal antibodies. It can also be used to diagnose and treat inflammatory disorders such as sepsis, fibrosis and arthritis and cancer pathologies such as adenocarcinomas and leukaemias
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1348 LHFVDQYREQLIARVTSVEVVLDKLHGQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDR 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; G-protein coupled receptor-8; GCREC-8; cytostatic; hepatotropic; virucide; antiniflammatory; anticonvulsant; antiemetic; neuroprotective; nootropic; cerebroprotective; hypotensive; tranquilliser; vulnerary; ophthalmological; cell proliferative disorder; actinic keratosis; anorectic; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; anorectic; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; psofiasis; cancer; neurological disorder; stroke, Alzhamer's disease; Huntington's disease; Parkinson's disease; cardiovascular disorder; epilepsy; hypertension; varicose vein; vasculitis; dysphagia; dyspepsia; anorexia; gastrointestinal disorder; pancreatitis; autoimmune disorder; Addison's disease; acquired immune deficiency syndrome; AlDS; uveitis; infection; transgenic animal; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LHFVDQYREQLIARVTSVEVVLDKLHGQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDR
                                                                                                                                                                                  Novel nucleic acid encoding NB-ARC and caspase associated recruitment domains, used to produce polypeptides for screening for modulators of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 490; DB 4; 100.0%; Pred. No. 2.2e-48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE06758 standard; protein; 1473
                           01-SEP-2000; 2000WO-US024152.
                                                        99US-00388221.
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                                                                                   BURN-) BURNHAM INST
                                                                                                                                         WPI; 2001-183258/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1442 AA;
                                                                                                                                                        N-PSDB; AAD02762
                                                        01-SEP-1999;
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                                                                                                                                                                                                                  apoptosis.
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                                                                                                              Reed JC;
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The present sequence is human G-protein coupled receptor-8 (GCREC-8)

C protein. The present invention relates to GCREC protein and nucleic acids

C concoling them. GCREC protein, its agonist or antagonist are useful for

C treating diseases or conditions associated with decreased expression or

C treating diseases or conditions associated with decreased expression or

C selected from cell proliferative disorders such as actinic keratosis,

arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, psoriasis,

arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, psoriasis,

ancer, neurological disorders such as epilepsy, stroke, Alzheimer's

C disease, Huntington's disease, parkinson's disease, cardiovascular

C disorders such as hypertension, vasculitis, varicose veins, gastro-

C intestinal disorders such as dysphagia, dyspepsia, anorexia, nausea,

Dancreatitis, autoimmune/inflammatory disorders such as acquired

C intestinal disorders such as dysphagia, dyspepsia, anorexia, nausea,

C intestinal disorders such as dysphagia, dyspepsia, corpus disease,

C intestinal disorders such as dysphagia, dyspepsia, craidiovascular

C intections, trauma and metabolic disorders such as diabetes, obesity,

C infections, trauma and metabolic disorders such as diabetes, obesity,

C cfreec copy is useful to create knock in humanised animals (pigs) or

C crangent animals (mice or rats) to model human disease, for therapeutic

C or diagnostic purposes, for somatic or germline gene therapy, to generate

C sequence, and in molecular biological techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LHFVDQYREQLIARVTSVEVVLDXLHGQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDR 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated human G-protein coupled receptor useful for diagnosing, preventing and treating cell proliferative, neurological, cardiovascular, gastrointestinal, autoimmune/inflammatory and metabolic disorders.
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                                        334. .341
/label= ATP/GTP-binding_site
/note= "P-loop"
1216. .1237
                                                                                                                                            1216. .1237
/label= Transmembrane domain
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cocation/Qualifiers
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11-FEB-2000; 2000US-0182045P.
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Best Local Similarity 100..
Then 95; Conservative
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                                                                                                                                                                                                                                                WO200157085-A2
       Key
Binding-site
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ID AAY7
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AC AAY7
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AAY72669;

Homo sapiens

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NB domain; nucleotide binding domain; NB-ARC and CARD;
           Human NB-ARC and CARD containing protein (NAC) beta isoform.
                                                                                                      129. .341
|label= Walker_A
'note= "Also designated as P-loop"
                                                                                                                                                                                                                    ue to alternative mRNA splicing"
                                                                                                                                                                                                                                note= "TIM-Barrel-like domain"
                                                                        location/Qualifiers
                                                                                                                       406. -414
/label= Walker_B
809. 833
/label= Leucine_ri
838. 862
/label= Leucine_ri
/label= Leucine_ri
                                                                                                                                                                                                                                      128. .1473
|abel= CARD-L
                                                                                                                                                                                                                                                        128. .1261
|abel= CARD-S
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                                                                                                                                                                                                                                                                                                                                                                                   99US-00388221
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'label= CAR
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/label= I.r.
75.
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/label= Let
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'label= Le
(first entry)
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N-PSDB; AAD02760.
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                                                            Homo sapiens
31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     apoptosis.
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The present sequence is a human NB-ARC and CARD containing protein (NAC)

beta isoform. NAC beta isoform represents the NAC splice variant in which

both the splice regions are present in the translated polypeptide. NAC

both the splice regions are present in the translated polypeptide. NAC

ARC domain, a caspase-associated binding (NB) domain (61so referred as NB-ARC domain), a caspase-associated recruitment domain (CARD) and a TIM-

ARC domain. The caspases, cysteine aspartyl proteases, are

principal effectors of apoptosis. CARD containing NAC proteins are used

for screening modulators that modulates apoptosis, cytckine production,

cytckine receptor signalling and other cellular processes. NAC can act as

an immunogen for the production of polyclonal and monoclonal antibodies.

It can also be used to diagnose and treat inflammatory disorders such as

sepsis, fibrosis and arthritis and cancer pathologies such as

sepsis, fibrosis and leukaemias. Note: This sequence is stated as being

the same as that shown as SRQ ID NO:2 (AAY72711) in figure 1A of the

specification. However the sequences differ at several positions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1379 LHFVDQYREQLIARVTSVEVVLDXLHCQVLSQEQYERVLAENTRPSQMRXLFSLSQSWDR 1438
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/label= NB_domain
/note=""Nucleotide binding domain, also designated as
NB_ARC domain"
329. .341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; NB domain; nucleotide binding domain; NB-ARC and CARD; NAC; caspase-associated recruitment domain; CARD; TIM-Barrel-like domain; cystelaine aspatryl protease; appotoals; cytokine production; cytokine receptor signaling; therapy; inflammatory disorder; sepsis; fibrosis; arthritis; cancer; adenocarcinoma; leukaemia.
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| Jabel= Walker_A
| note= "Also designated as P-loop
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100.0%; Pred. No. 2.3e-48;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KCKDGLYQALKETHPHLIMELWEKGSKKGLLPLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human NAC beta isoform, alternative version.
               Claim 15; Page 133-137; 184pp; English.
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/label= I.c
38
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/label= W-7
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/label= Let
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/label= Le
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  957. 987
/note= "This 31 amino acid segment is not found in NAC
gamma isoform (AAY72670) and NAC delta isoform (AAY72671)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   not found in NAC
                                                                                                                                                                                                                                          /note= "Nucleotide binding domain, also designated as NB ARC domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acid encoding NB-ARC and caspase associated recruitment domains, used to produce polypeptides for screening for modulators of
                                                                                   caspase-associated recruitment domain; CARD; IIM-Barrel-like domain; cysteine aspartyl protease; apoptosis; cytokine production; cytokine receptor signalling; therapy; inflammatory disorder; sepsis; fibrosis; arthritis; cancer; adenocarcinoma; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1261. .1306
/note= "This 45 amino acid segment is not found igamma isoform (AAY72670) due to alternative mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Caspase-associated recruitment domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306. .1473
|abel= CARD-S
note= "Caspase-associated recruitment domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Caspase-associated recruitment domain"
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Leucine_rich_repeat_region

Leucine_rich_repeat_region

Leucine_rich_repeat_region Leucine_rich_repeat_region Leucine_rich_repeat_region

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domain (also referred as NB-ARC domain), a caspase-associated recruitment domain (CARD) and a TIM-Barrel-like domain. The caspases, cysteine aspartyl proteases, are principal effectors of apoptosis. CARD containing NAC proteins are used for screening modulators that modulates apoptosis, cytokine production, cytokine receptor signalling and other cellular processes. NAC can act as an immunogen for the production of polyclonal and monoclonal antibodies. It can also be used to diagnose and treat inflammatory disorders such as sepsis, fibrosis and arthritis and cancer pathologies such as adenocarcinomas and leukaemias. Note: This sequence is stated as being the same as that shown as SRQ ID NO:2 (See AAY72669) in page 113-137 of the specification. However the sequences differ at
/note= "This 31 amino acid segment is not found in NAC gamma isoform (AAY72670) and NAC delta isoform (AAY72671) due to alternative mRNA splicing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a human NB-ARC and CARD containing protein (NAC) beta isoform, alternative version. NAC beta isoform represents the NAC splice variant in which both the splice regions are present in the translated polypeptide. NAC protein comprises a nucleotide binding (NB)
                                                                                                                                                                                                     in NAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid encoding NB-ARC and caspase associated recruitment domains, used to produce polypeptides for screening for modulators of
                                                                                                                                                                                                     /note= "This 45 amino acid segment is not found :
gamma isoform (AAY72670) due to alternative mRNA
                                                                                                                 note= "Caspase-associated recruitment domain"
128. 1261
|abel= CARD-S
                                                                                                                                                                     note= "Caspase-associated recruitment domain"
                                                                                                                                                                                                                                                                                                                    note= "Caspase-associated recruitment domain"
                                                                                                                                                                                                                                                                                                                                                                        note= "Caspase-associated recruitment domain"
                                                                                                                                                                                                                                                    1298. .1305
/note= "Encoded by GGGATGCTGGAAATACTCCCCAAG"
                                                   1079. .1364
/note= "TIM-Barrel-like domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 15; Fig 1A; 184pp; English.
                                                                                   128. .1473
label= CARD-L
                                                                                                                                                                                                                                                                                                      CARD-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-SEP-2000; 2000WO-US024152.
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                                                                                                                                                                                                                                                                                                                                      373. .1473 
label= CARD
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N-PSDB; AAD02760.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           apoptosis.
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                                                     Domain
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                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                      Domain
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1439 KCKDGLYQALKETHPHLIMELWEKGSKKGLLPLSS 1473
                    셤
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Search completed: July 28, 2004, 08:53:00 Job time : 56.9398 secs

Query Match

Sequence 1473 AA;

o O 100.0%; Score 490; DB 4; Length 1473; 100.0%; Pred. No. 2.3e-48; 0; Mismatches 0; Indels 0 Conservative Best Local Similarity Matches 95; Conserv

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9

61 KCKDGLYQALKETHPHLIMELWEKGSKKGLLPLSS 95

1379 LHFVDQYREQLIARVTSVEVVLDKLHGQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDR 1438

g à

1 LHFVDQYREQLIARVTSVEVVLDKLHGQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDR

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

July 28, 2004, 08:46:11 ; Search time 41.0602 Seconds (without alignments) 488.572 Million cell updates/sec Run on:

US_09-996-617-8_COPY_111_181 Title: Perfect score:

378 1 GLHFIDQHRAALIARVTNVE.....LFSFTPAWNWTCKDLLLQAL 71 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

Total number of hits satisfying chosen parameters: 1586107 seqs, 282547505 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_29Jan04:* 1: geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	Aae00594 Alternati		Human	Human	Human		Pyrin	5 Human	7 Human	1 Human	Aae00593 Rat targe	Aab20086 Mouse CAR		Mouse	Human			Abg78455 Human cas	Abg78472 Leucine-r	Abb77916 Human leu	Abq97969 Human leu	5 Pyrin	Human		Human
SUMMANIES	ΩI	AAE00594	AAY48553	AAU68525	AAB20085	AAE00588	AAU99353	AA017854	ABG71635	AAG74647	AAE00591	AAE00593	AAB20086	AAE00592	AAU99352	AAB24513	AAY72670	AAB62571	ABG78455	ABG78472	ABB77916	ABG97969	AA017855	ABG71631	ABP96889	ABP96888
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æ	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	98.4	ä	69.8	8.69	8.69	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1
	Score	378	378	378	378	378	378	378	378	378	372	275	264	264	264	216	216	216	216	216	216	216	216	216	216	216
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Abg71633 Human cas Aay72671 Human NB- Aae06758 Human G-p Aay72669 Human NB-	Human Human Human	Aab24519 Human sec Aab24520 Human sec Abj04755 ARC prote		Adc46453 Human neo Aab62572 Human CAR Aay72672 Human CAR	Abu03496 Angiogene Abg71632 Human cas Abb82736 Human TUC Abg71634 Human cas
ABG71633 AAY72671 AAE06758 AAY72669	AAY72711 AAG74648 AAB43675	AAB24519 AAB24520 ABJ04755	ABR58613 ADD48044 AAU21812	ADC46453 AAB62572 AAY72672	ABU03496 ABG71632 ABB82736 ABG71634
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1429 1442 1473	1473 158 190	9 22 6 8 23 6 8	208 219 230	230 431 431	431 431 431
57.1 57.1 57.1 57.1	. 66	37.3 19.8 18.4	18.4 18.4 18.1	181	18:1 18:1 18:1 18:1
216 216 216 216	216 214 214	141 75 69.5	69 69 69 50 50 50	68 68.5 68.5 7	68888 68555
28 28 29 29	30 32 32	3 3 3 3 4 3	36 38 38	34 40 10	4 4 4 4 2 6 4 7 5

ALIGNMENTS

RESULT 1

Human, target of methylation-induced silencing-1; TMS1, cytostatic; antiproliferative; apoptosis inducer; gene therapy, CpG island; caspase-recruiting domain, CARD, cancer; breast. Alternatively spliced form of human TMS1 protein (lacking exon2). AAE00594 standard; protein; 176 AA. (first entry) 02-JUL-2001 AAE00594; AAE00594

WO200129235-A2. Homo sapiens.

26-APR-2001

18-OCT-2000; 2000WO-US028747.

99US-0159975P. 18-OCT-1999;

(UYEM-) UNIV EMORY.

Vertino PM;

WPI; 2001-290922/30. N-PSDB; AAD03906 Novel gene TMS1, transcriptionally silenced due to increased methylation useful for identifying subject at risk of developing tumor characterized by abnormal methylation, for treating cancer by inducing apoptosis.

Claim 85; Page 123; 124pp; English.

The invention relates to identification of target of methylation-induced abnormal methylation of a CpG island in its 5' regulatory region. TMS1 sensitives of a carboxy terminal caspase-recruiting domain (CARD) and plays a role in induction of apoptosis. TMS1 gene and protein are useful as tools for diagnosing and treating a subject at risk of developing cancer (e.g. breast cancer) characterised by abnormal CpG methylation or abnormally low levels of TMS1 expression products. Unique fragments of TMS1 gene are used as probes. TMS1 gene is useful in gene therapy. TMS1 molecule is also useful for treating abnormal cell proliferation by increasing TMS1 polypeptide level to an above normal level. The CpG

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111 GLHFIDQHRAALIARVTNVEWLLDALYGKVLTDEQYQAVRAEPTNPSKMRKLFSFTPAWN 170
                                                                                                                                                                                                                                                                                                     AAU68525;
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AAU68525
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                                                                                                                                                                                                                                                                                                                                                          92 GLHFIDQHRAALIARVINVEWLLDALYGKVLTDEQYQAVRAEPINPSKMRKLFSFTPAWN 151
                                                                                                                                                                                                                                                                                                           9
             island region of TMS1 or its fragments are used to study the methylation patterns apart from any coding region contained in it. The present sequence is alternatively spliced form of human target of methylation-induced silencing-1 (TMS1) protein lacking exon2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosentahl A;
                                                                                                                                                                                                                                                                                                           1 GLHFIDQHRAALIARVTNVEWLLDALYGKVLTDEQYQAVRAEPTNPSKMRKLFSFTPAWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human nucleic acid sequences and protein products from tumor breast tissue, useful for breast cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expressed sequence tag; EST; human; breast; cancer; gene therapy; treatment; tumour; cytostatic; medicament.
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0
                                                                                                                                                                                                      Length 176;
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                                                                                                                                                                                                                                                           Indels
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Best Local Similarity 100.0%; Pred. No. 3.7e-40;
Matches 71; Conservative 0; Mismatches 0;
                                                                                                                                                                                                      100.0%; Score 378; DB 4;
100.0%; Pred. No. 3.2e-40;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schmitt A, Pilarsky C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human breast tumour-associated protein 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY48553 standard; protein; 195 AA.
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                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 22; 149; 188pp;
                                                                                                                                                                                                                                                                                                                                                                                                                       61 WTCKDLLLQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-528981/45.
N-PSDB; AAZ33631.
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                                                                                                                                                      Sequence 176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY48553;
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The invention relates to isolated human polypeptides (which may be cytokines) and the polynucleotides encoding them. The protein is useful for identifying a compound which binds to it (e.g. modhlators) agonists. and matagonists). The polynucleotides are useful as an array for mismatch detection. The protein exhibits exhibits activity relating to cytokine, cell proliferation, cell differentiation, antiniflammatory, stem cell growth factor activity, immune stimulating or immune suppressing and activin or inhibin related activities. The proteins (and antibodies raised against them) and nucleic acids are therefore useful in the diagnosis and treatment of diseases and disorders such as cancer, central and peripheral nervous system diseases and neuropathies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptides and nucleic acids, useful for diagnosis, treatment of inflammatory, autoimmune, neurological, myeloid or lymphoid cell, bone degenerative disorders, cancer and promoting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                   periodontal disease; fibrosis; reperfusion; immune disorder; SCID; severe combined immunodeficiency; infection; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; allergy; asthma; coagulation disorder; haemophilia; sepsis; nephritis; inflammatory bowel disease; food supplement; immunogen.
                                                                                                                                                                                                                                                                                Human, cytokine, cell proliferation, cell differentiation; antiinflammatory, stem cell growth factor; activin; inhibin; cancer; nervous system disease; neuropathy, Alzheimer's disease; neuropathy, Parkinson's disease; Humington's disease; spinal cord disorder; head trauma; stroke; myeloid cell disorder; lymphoid cell disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang J;
Liu C;
                                                                                                                                                                                                                                                                                                                                                                          platelet disorder; thrombocytopaenia; stem cell disorder; aplastic anaemia; tissue regeneration; wound healing; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P, Xue AJ, Ren F, Zhang J,
Chen R, Wang D, Goodrich RW,
                                                                                                                                                                                                                                            Human novel cytokine encoded by cDNA 790CIP2B_1 #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Page 242-243; 336pp; English.
                                                                                                                                  AAU68525 standard; protein; 195 AA.
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30-NOV-2000; 2000US-00728711.
14-MAR-2001; 2001US-00808701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US010484.
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22-SEP-2000; 2000US-00668680.
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, Yang Y, Zaho QA,
                                                                                                                                                                                                               (first entry)
                            171 WTCKDLLLQAL 181
77
  61 WTCKDLLLQAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000;
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Indels

Length 195;

Claim 9; Fig 21; 208pp; English.

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Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic disteral sclerosis, spinal cord disorders, head trauma, cerebrovascular diseases, stroke, myebloid or lymphoid cell disorders, platelet disorders, thrombocytopaenia, stem cell disorders, aplastic anaemia, for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, lung or liver fibrosis, reperius injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders (e.g. multiple sclerosis, rebumatoid arthritis, diabetes mellitus, myasthenia gravis), allergic reactions and conditions, such as asthma or other respiratory problems, coagulation disorders, haemophila), septic shock, sepsis, arthritis, nephritis and inflammatory cohercetistics. The present sequence represents a novel protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 195 AA;
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GLHFIDQHRAALIARVINVEWLLDALYGKVLTDEQYQAVRAEPTNPSKWRKLFSFTPAWN 170
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                                                            1 GLHFIDQHRAALIARVTNVEWLLDALYGKVLTDEQYQAVRAEPTNPSKMRKLFSFTPAWN
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       Length 195;
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      100.0%; Score 378; DB 4;
100.0%; Pred. No. 3.7e-40;
ive 0; Mismatches 0;
                                  Conservative
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Query Match
Best Local Similarity
Matches 71; Conserv
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WICKDLLLOAL 181 171

AAB20085 standard; protein; 195 AA. AAB20085; AAB20085 RANGE STATE OF STATE

(first entry) 23-APR-2001

Human CARD-5 protein.

CARD-5; caspase recruitment domain; human; cancer; infection; autoimmune disease; neurological disease; haematological disease; immunomodulator; antiseptic; immunomodulator; antiinflammatory; apoptosis; diagnosis; gene therapy.

Homo sapiens

Location/Qualifiers 111. .181 /note= "CARD" Domain

WO200100826-A2

28-JUN-2000; 2000WO-US017691. 04-JAN-2001

99US-00340620. 28-JUN-1999;

(MILL-) MILLENNIUM PHARM INC

Bertin J;

WPI; 2001-061973/07. N-PSDB; AAF30007

Isolated intracellular proteins predicted to be involved in regulating caspase activation are used for diagnosis and treatment of e.g. cancer, viral infections, autoimmune diseases, neurological diseases and hematological disorders.

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The present sequence is that of human caspase recruitment domain 5 (CARD-5), an intracallular protein predicted to be involved in regulating caspase activation. The sequence is predicted from an isolated curva clone (see AAF3007). Methods of diagnosing and treating patients suffering from a disorder associated with an abnormal level or rate of apoptotic cell death, abnormal activity of the Fas/APO-1 receptor complex, abnormal activity of the tumour necrosis factor receptor complex, abnormal activity of a caspase involve administering a compound that modulates the activity of activity of CARD-4, CARD-5 or CARD-6. Seq. using central manner disorders include cancer, viral infection, autoimmune disorders include cancer, viral infection, autoimmune disorders include cancer, viral infection, configuratory disorders and immune disorders. CARD-3, -4, -5 and -6 proteins can be used to regulate cell proliferation, cell survival and cell growth. They can also be used to screen drugs or compounds that compute their activity or expression and to treat disorders associated with insufficient or excessive production of CARD-3, -4, -5 or -6 protein, or production of an aberrant protein
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Human, target of methylation-induced silencing-1, TMS1, cytostatic, antiproliferative, apoptosis inducer, gene therapy, CpG island, caspase-recruiting domain, CARD, cancer, breast. Human target of methylation-induced silencing-1 (TMS1) protein. 02-JUL-2001 (first entry) AAE00588;

AAE00588 ID AAE00588 standard; protein; 195 AA.

RESULT 5

Homo sapiens

WO200129235-A2.

26-APR-2001.

18-OCT-2000; 2000WO-US028747.

99US-0159975P 18-OCT-1999;

(UYEM-) UNIV EMORY.

Vertino PM;

WPI; 2001-290922/30. N-PSDB; AAD03889, AAD03890.

Novel gene TWS1, transcriptionally silenced due to increased methylation useful for identifying subject at risk of developing tumor characterized by abnormal methylation, for treating cancer by inducing apoptosis.

Claim 85; Page 114; 124pp; English

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silencing-1 (TMS1) gene. This gene is transcriptionally silenced due to abnormal methylation of a CpG island in its 5' regulatory region. TMS1 consists of a carboxy terminal caspase-recruiting domain (CARD) and plays a role in induction of apoptosis. TMS1 gene and protein are useful as tools for diagnosing and treating a subject at risk of developing cancer (e.g. breast cancer) characterised by abnormal CpG methylation or abnormally low levels of TMS1 expression products. Unique fragments of TMS1 gene are useful in gene therapy. TMS1 molecule is also useful for treating abnormal cell proliferation by increasing TMS1 polypeptide level to an above normal level. TMC CpG island region of TMS1 or its fragments are used to study the methylation patterns apart from any coding region contained in it. The present sequence is human target of methylation-induced silencing-1 (TMS1)
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The invention relates to identification of target of methylation-induced
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/label= CARD domain
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control of the control of the control of candary of murine and human caspase recruitment domain (CARD)-5. Caspases caids, of murine and human caspase recruitment domain (CARD)-5. Caspases corporates and caspases are central to the apoptotic caspases interact with other caspases via their CARDs and different caspases interact with other caspases via their CARDs and different caspases interact with other caspases via their CARDs and different caspases interact with other caspases via their CARD-5 is an intracellular protein that is predicted to be involved in regulating intracellular protein that is predicted to be involved in regulating caspase activation. CARD-5 activates the nuclear factor-kappa B (NF-CARD-7 and itself CARD-5 can, therefore, modulate CARD-5 activity and repapable is the CARD-5 can, therefore, modulate CARD-5 activity and control of the protein to them and modulate their activity and for cappable antibodies and and modulate their activity and for detecting the presence of CARD-5 in a sample. CARD-5 polypeptides, can be used to treat immune disorders such as asthma and allenty, glamerular disorders, antibodies and modulaters of CARD-5 polypeptides.

CC an be used to treat immune disorders such as chronic inflammatory diseases and disorders, Habimoto's thyroiditis, graft rejection, carcidosis, atopic conditions (such as asthma and allensy), glomerular compluing tuberculosis and lepromatous leprosy) and in screening and chection assays. Modulators of CARD-5 activity or expression are also expension and arthritis, cell depletion, neurological disorders, such as systemic lupus creating autoimmune disorders, such as systemic lupus contentions and arthritis, cell depletion, neurological disorders, such as mychomera's such as any dispase, such as mychopic and appartic such an emphasic such as any end and appartic managemental muscular artophy, and ansense and appartic such as any end and appartic such an emphasic such as any end and appartic such an emphasized such as any end and appartic such an empha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             haematologic diseases, such as myelodysplastic syndrome and aplastic anaemia, myocardial infarction and stroke. The sequence presented is the human caspase recruitment domain-5 (CARD-5) protein
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                                                          Novel isolated murine or human caspase recruitment domain (CARD)-5 polypeptide, useful for treating immune disorders such as Hashimoto's thyroiditis, graft rejection, allergy, glomerular nephritis,
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100.0%; Pred. No. 3.7e-40;
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                                                                                                                                                                                                Claim 22; Fig 3; 100pp; English.
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2002-557538/59.
                          N-PSDB; ABK87966
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                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates the DNA and their encoded proteins, where the proteins contain at least one PYD (pyrin) domain. These can be used to treat diseases associated with impaired intracellular signal transduction, particularly inflammation such as psoriasis, arteriosclerosis, bacterial or viral infections (particularly meningitis art premental, multiphe sclerosis, rheumatoid arthritis, asthma, sarcoidosis, glomerulonephritis and osteoarthritis, and also Alzheimer's and Parkinson's diseases. The present sequence is a protein of the
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                                                                                                                                                                                                                                                                                                                     otein with pyrin domain, useful for treating diseases signal transduction, particularly inflammation, also
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Matches 71; Conservative 0; Mismatches 0; Indels C
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                                                                                                                                                                                                                                                                                                                   New DNA encoding protein with involving impaired signal tran proteins and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Fig 1; 116pp; German.
                                                                                                                                                                                   (APOT-) APOTECH RES & DEV LTD
                                                                                                                             15-NOV-2000; 2000DE-01056687.
                                                                                       30-OCT-2001; 2001WO-EP012545.
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The present invention relates to methods of identifying compounds that regulate caspase activity using caspase recruitment domain-7 (CARD-7) or caspase recruitment domain-8 (CARD-8). In particular, a method for identifying a compound that modulates the interaction between CARD-8 and caspase-1, pseudo-interleukin-1 (IL-1) beta converting enzyme (pseudoICE) or ICEBERG is disclosed. CARD-7 and CARD-8 molecules are useful as methods in regulating a variety of cellular processes including cell growth, cell death, and inflammation. The methods of the invention are useful for identifying compounds that have the ability to induce caspase of increase/decrease apoptosis, or comprise the ability to induce caspase activation. The methods are useful for treating a disorder associated with inappropriate apoptosis or inappropriate inflammation. The methods of vith inappropriate apoptosis or inappropriate inflammation. The methods are useful for treating a disorder associated with inappropriate apoptosis or inappropriate inflammation. The methods of vital infections, autoinfmune diseases caused by low levels of apoptosis or viral infections, autoinfmune diseases caused by low levels of apoptosis (e.g. systemic lupus erythematosus, immune-mediated glomerulonephritis, and arthritis). The methods are also useful for treating disorders with undesirably high rates of apoptosis such as human immunodeficiency virus (HIV) infection, Alzheimer's disease, Parkinson's disease, amylotrophic aleras sciences for propertion anamnia associated with chronic virus forms of cerebellar degeneration, anamnia associated with chronic virus forms of cerebellar degeneration, anamnia associated with chronic virus forms of methods are also useful for treating diseases are also were the above the apoptosis of apoptosis such as mania associated with chronic virus forms of cerebellar degeneration, anamnia associated with chronic virus forms of the properties of apoptosis of the properties of apoptosis of the properties of apoptosis of the properties of apo
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Identifying modulator of CARD-7 and CARD-5 interaction, by contacting CARD-7 and CARD-5 in presence of test compound, measuring their binding, and identifying modulator, when binding of CARD-7 to CARD-5 is altered.

WPI; 2003-028967/02. N-PSDB; ABS56032.

27-NOV-2001; 2001US-00996617.

US2002128198-A1. Homo sapiens.

12-SEP-2002

28-JUN-1999; 99US-00340620. 27-OCT-1999; 99US-00428252. 15-AUG-2001; 2001US-00931071.

(BERT/) BERTIN J.

Bertin J;

AAG74647 ID AAG7 RESULT 9

AAG74647 standard; protein; 205 AA.

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The invention relates to identification of target of methylation-induced silencing-1 (TMS1) gene. This gene is transcriptionally silenced due to cahornal methylation of a CpG island in its 5' regulatory region. TMS1 consists of a carboxy terminal caspase-recruiting domain (CARD) and plays a role in induction of apoptosis. TMS1 gene and protein are useful as a role in induction of apoptosis. TMS1 gene and protein are useful as abnormally low levels of TMS1 as subject at risk of developing cancer (e.g. breast cancer) characterised by abnormal CPG methylation or abnormally low levels of TMS1 expression products. Unique fragments of TMS1 gene are used as probes. TMS1 gene is useful in gene therapy. TMS1 molecule is also useful for treating abnormal cell proliferation by increasing TMS1 polypeptide level to an above normal level. The CpG increasing TMS1 polypeptide level to an above normal level. The CpG patterns apart from any coding region contained in it. The present sequence is human target of methylation-induced silencing-1 (TMS1) exon3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 THEIDQHRAALIARVINVEWLEDALYGKVLTDEQYQAVRAEPTNPSKMRKLFSFTPAWNW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel gene TMS1, transcriptionally silenced due to increased methylation useful for identifying subject at risk of developing tumor characterized by abnormal methylation, for treating cancer by inducing apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LHFIDQHRAALIARVTNVEWLLDALYGKVLTDEQYQAVRAEPTNPSKMRKLFSFTPAWNW
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                                        Human target of methylation-induced silencing-1 (TMS1) exon3 protein.
                                                                                    Human; target of methylation-induced silencing-1; TMS1; cytostatic; antiproliferative; apoptosis inducer; gene therapy; CpG island; caspase-recruiting domain; CARD; cancer; breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat; target of methylation-induced silencing-1; TMS1; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.4%; Score 372; DB 4; I
100.0%; Pred. No. 7.5e-40;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 25; Page 117; 124pp; English
                                                                                                                                                                                                                                                                                                                                    18-OCT-2000; 2000WO-US028747.
                                                                                                                                                                                                                                                                                                                                                                                       99US-0159975P.
(first entry)
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N-PSDB; AAD03894.
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nes 70; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 84 AA;
                                                                                                                                                                                                                                           WO200129235-A2
                                                                                                                                                                                                                                                                                                                                                                                       18-OCT-1999;
                                                                                                                                                                                             Homo sapiens
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  02-JUL-2001
                                                                                                                                                                                                                                                                                         26-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cancer-associated nucleic acid molecules (N) and proteins (P), where the cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens the colon cancer antigens the colon cancer antigens have cytostatic activity and can be used in gene therapy and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome contract affect the activity of P by expressing inactive proteins or to that affect the activity of P by expressing inactive proteins or to cample ment the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinems and cancers. AAH37196 to AAH37704 and AAB77789 represent sequences used in the exemplification of the present invention. N B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GLHFIDQHRAALIARVTNVEWLLDALYGKVLTDBQYQAVRAEPTNPSKMRKLFSFTPAWN
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                                                                                                                                                                           Human; colon cancer; colon cancer antigen; diagnosis; detection;
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100.0%; Pred. No. 3.9e-40;
.ive 0; Mismatches 0; Indels
                                                                                                                        Human colon cancer antigen protein SEQ ID NO:5411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 7035-7036; 9803pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0157137P.
                                                                                                                                                                                                                                                                                                                                                                                               28-SEP-2000; 2000WO-US026524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                          (first entry)
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                                                                                                                                                                                                    colorectal carcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 71; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 205 AA;
                                                                                                                                                                                                                                                                                              WO200122920-A2
                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                             29-SEP-1999;
03-NOV-1999;
                                                                               03-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM,
                                 AAG74647;
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Gaps

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RESULT 10

à g ò AAE00591 ID AAE(XX AC AAE(XX

Length 84; 0; Indels

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The present sequence is that of mouse caspase recruitment domain 5 (CARD-S), an intracellular protein predicted to be involved in regulating caspase activation. The sequence is predicted from an isolated cDNA clone (see AAF30008). It shows 71.8% amino acid identity to human CARD-5 (see AAF30008). Methods of diagnosing and treating patients suffering from a clisordar associated with an abnormal level or rate of apoptoric cell death, abnormal activity of the FaAPA00-1 receptor complex, abnormal activity of the FaAPA0-1 receptor complex, abnormal activity of the sappase involve administering a compound that modilates the expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6 e.g. using catolimized activity of CaRD-3, cancer, viral infection, catolimman disorders and immune disorders include cancer, viral infection, ciliammatory disorders and immune disorders. An enactological disorders, ciliammatory disorders and immune disorders. At -5 and -6 coll growth. They can also be used to screen drugs or compounds that modulate their activity or expression and to treat disorders associated with insufficient or excessive production of CARD-3, -4, -5 or -6 protein, or production of an aberrant protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated intracellular proteins predicted to be involved in regulating caspase activation are used for diagnosis and treatment of e.g. cancer, viral infections, autoimmune diseases, neurological diseases and
    immune disease; inflammation; antitumour; antiseptic; immunomodulator; antiinflammatory; apoptosis; diagnosis; gene therapy.
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Pred. No. 1.6e-25;
7; Mismatches 11; Indels
                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Fig 19; 208pp; English.
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1 Similarity 73.9%;
51; Conservative 7
                                                                                                                                                                                                                                                                                                                                             99US-00340620
                                                                                                                                                                                                                                                                                               28-JUN-2000; 2000WO-US017691
                                                                                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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N-PSDB; AAF30008.
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                                                                                                                                                                                                       WO200100826-A2
                                                                                                                                                                                                                                                                                                                                             28-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Bertin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171
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                                                                       Mus sp
                                                                                                                                        Domain
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                                                                                                                   Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to identification of target of methylation-induced ablormal (TMS1) gene. This gene is transcriptionally silenced due to abnormal methylation of a CpG island in its 5' regulatory region. TMS1 consists of a carboxy teminal caspase-recruiting domain (CARD) and plays a role in induction of apoptosis. TMS1 gene and protein are useful as tools for diagnosing and treating a subject at risk of developing center (e.g. breast cancer) characterised by abnormal CpG methylation or abnormally low levels of TMS1 expression products. Unique fragments of TMS1 gene are used as probes. TMS1 gene is useful in gene therapy. TMS1 molecule is also useful for treating abnormal cell proliferation by increasing TMS1 ploypeptide level to an above normal level. The CpG island region of TMS1 or its fragments are used to study the methylation patterns apart from any coding region contained in it. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel gene TMS1, transcriptionally silenced due to increased methylation useful for identifying subject at risk of developing tumor characterized by abnormal methylation, for treating cancer by inducing apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 HFIDOHRAALIARVTNVEWLLDALYGKVLTDEQYQAVRAEPTNPSKMRKLFSFTPAMNWT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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gene therapy; CpG island;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.8%; Score 275; DB 4; Length 171; 76.8%; Pred. No. 5.4e-27; ive 6; Mismatches 10; Indels
antiproliferative; apoptosis inducer; gene thers
caspase-recruiting domain; CARD; cancer; breast.
                                                                                                                                                         /note= "Encoded by AGY"
                                                                                               Location/Qualifiers Misc-difference 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 85; Page 121; 124pp; English.
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                                                                                                                                                                                                                                                                                           18-OCT-2000; 2000WO-US028747
                                                                                                                                                                                                                                                                                                                                        99US-0159975P
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Matches 53, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-290922/30.
                                                                                                                                                                                                                                                                                                                                                                                   (UYEM-) UNIV EMORY.
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CKNLFLEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CKDLLLQAL
                                                                   Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAD03905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 171 AA;
                                                                                                                                                                                                  WO200129235-A2
                                                                                                                                                                                                                                                                                                                                        .8-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Vertino PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
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proliferation; gene therapy; immune disorder;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                              Novel gene TMS1, transcriptionally silenced due to increased methylation useful for identifying subject at risk of developing tumor characterized by abnormal methylation, for treating cancer by inducing apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 HFIDQHRAALIARVTNVEWLLDALYGKVLTDEQYQAVRAEPTNPSKWRKLFSFTPAWNWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse; caspase recruitment domain-5; CARD-5; antiinflammatory; immunosuppressive; caspase; cysteinyl aspartate-specific proteinase; apoptosis; nuclear factor-kappa B; NF-kappaB; transcription factor;
                             Mouse; target of methylation-induced silencing-1; TMS1; cytostatic; antiproliferative; apoptosis inducer; gene therapy; CpG island; caspase-recruiting domain; CARD; cancer; breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
Mouse target of methylation-induced silencing-1 (TMS1) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.8%; Score 264; DB 4; Length 193; 73.9%; Pred. No. 1.6e-25; ive 7; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse caspase recruitment domain-5 (CARD-5) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU99352 standard; protein; 193 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 85; Page 120; 124pp; English
                                                                                                                                                                                                             18-OCT-2000; 2000WO-US028747.
                                                                                                                                                                                                                                          99US-0159975P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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N-PSDB; AAD03904.
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                                                                                                                                                                                                                                                                               (UYEM-) UNIV EMORY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 193 AA;
                                                                                                                                          WO200129235-A2
                                                                                                                                                                                                                                              18-OCT-1999;
                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-OCT-2002
                                                                                                                                                                            26-APR-2001
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The invention discloses the isolated polypeptides, and encoding nucleic acids, of murine and human caspase recruitment domain (CARD)-5. Caspases (Cysteinyl aspartate-specific proteinases) are central to the apoptotic crospases interact with other caspases via their CARDs and different lead to the morphological changes seen in cells undergoing apoptosis. Caspases sinteract with other caspases via their CARDs and different cubrypes of CARDs may confer binding specificity. CARD-5 is an intracellular protein that is predicted to be involved in regulating caspase activation. CARD-5 activates the nuclear factor reappa B (NF-CARD-7 and itself. CARD-5 can, therefore, modulate CARD-5 activity and NF-CARD-7 and itself. CARD-5 can, therefore, modulate CARD-5 activity and centenging the presence cell growth and cell death and be used in compounds which bind to them and modulate their activity and for compounds which bind to them and modulate their activity and for can be used to treat immune disorders such as chronic inflammatory diseases and disorders. Hashimoro's thyroiditis, graft rejection, diseases and disorders. Hashimoro's thyroiditis, graft rejections conditions (such as asthma and allergy), glomerular ceptuiding tuberculosis and lepromatous leprosy) and in screening and detection assays. Modulators of CARD-5 activity or expression are also useful for treating autoimmune disorders, such as systemic lugues crythematosus and arthritis, cell depletion, neurological disorders, such as myelodysplastic syndrome and applastic characterial infarmacoular atrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cologic diseases, such as myelodysplastic syndrome and aplastic a, myocardial infarction and stroke. The sequence presented is the caspase recruitment domain-5 (CARD-5) protein
             graft rejection;
                                                                     lepromatous leprosy, autoimmune disorder; systemic lupus erythematosus; arthritis; cell depletion; neurological disorder; Alzheimer's disease; Parkinson's disease; spinal muscular atrophy; haematologic disease; myelodysplastic syndrome; aplastic anaemia; myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated murine or human caspase recruitment domain (CARD)-5 polypeptide, useful for treating immune disorders such as Hashimoto's thyroiditis, graft rejection, allergy, glomerular nephritis,
      chronic inflammatory disease; Habimoto's thyroiditis; graft rejection sarcoidosis; atopy; asthma; allergy; glomerular nephritis; human immunodeficiency virus; HIV; bacterial infection; tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.8%; Score 264; DB 5;
llarity. 73.9%; Pred. No. 1.6e-25;
Conservative 7; Mismatches 11;
                                                                                                                                                                                                                                                                     110. .193
/label= CARD domain
                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 22; Fig 1; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2000; 2000US-00728721.
24-APR-2001; 2001US-00841879.
                                                                                                                                                                                                                                                                                                                                                                                                                      29-NOV-2001; 2001WO-US044894.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MILL-) MILLENIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-557538/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity.
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABK87964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 193 AA;
                                                                                                                                                                                                                                                                                                                                   WO200244354-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                              06-JUN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bertin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                  stroke.
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Gaps ·. 61

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The polymucleotide sequence given in AAA78381 to AAB24604. Human secreted human secreted proteins given in AAB24437 to AAB24604. Human secreted proteins given in AAB24437 to AAB24604. Human secreted proteins have activities based on the tissues and calls the genes are expressed in Examples of activities include: cytostatic; antianaemic; antidiabetic; antiinflammatory; ophthalmological; antirheumatic; antidiabetic; antiporatitic; antimicrobial and antiparkinsonian. Human secreted protein polynucleotides, polypeptides, antagonists and/or agonists may be useful in treating, preventing, and/or diagnosing other disorders and/or conditions such as: (a) cancers; (b) disorders of the immune system; (c) angiotogenesis disorders; (b) disorders of the immune system; (c) angiotogenesis disorders; (f) diseases associated with increase apoptosis; (g) neurological diseases; and (n) infectious diseases. They are also used to promote wound healing.

AAA78372 to AAA78380 and AAB24436 represent sequences used in the exemplification of the present invention
Forty seven human nucleic acids encoding secreted proteins, useful in the treatment, prevention and diagnosis of cancers, disorders of the immune system, anglogenesis disorders, neurological diseases and hyperproliferative disorders.
                                                                                                                                                                                                                                                                                                                                                            Human; secreted protein; cytostatic; antianaemic; antidiabetic; antiinflammatory; ophthalmological; antirheumatic; antiarthritic; antiparamatory; ophthalmological; anti-heumatic; antiangiogenic; cardiant; anti-HIV; nootropic; neuroprotective; antimicrobial; antiparkinsonian; cancer; mimune system disorder; angiogenesis; hyperproliferative disorder; apoptosis; neurological disease; infectious disease; wound healing.
                                                                                                                                                                                                                                                                                                                          Human secreted protein sequence encoded by gene 12 SEQ ID NO:139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA, Endress GA, Soppet DR, Ni J;
Shi Y, Lafleur DW, Olsen HS, Florence K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 37; 562pp; English.
                                                                                                                                                                                                            AAB24513 standard; protein; 442 AA.
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98US-0113006P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US029950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                      20-NOV-2000 (first entry)
                                                                                                      171 CKDSLLQAL 179
                                                                            71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruben SM, Ebner R,
Duan DR, Moore PA,
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                                                                          CKDLLLQAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200035937-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-DEC-1999;
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18-DEC-1998;
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DB 3; Length 442;

57.1%; Score 216;

Query Match

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339 IHFVDQYREQLIARVISVEVVLDKLHGQVLSQEQYERVLAENTRPSQMRKLFSLSQSWDR 398
                                                                    2 LHFIDQHRAALIARVTNVEWLLDALYGKVLTDEQYQAVRAEPTNPSKMRKLFSFTPAWNW
Best Local Similarity 61.4%; Pred. No. 6.8e-19;
Matches 43; Conservative 12; Mismatches 15; Indels
                                                                                                                                                                                                                                                                        Search completed: July 28, 2004, 08:53:00 Job time: 41.0602 secs
                                                                                                                                                                                                        399 KCKDGLYOAL 408
                                                                                                                                                            62 TCKDLLLQAL 71
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CRGANISM: Homo sapiens
US-09-340-620A-58
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RESULT 1
US-09-340-620A-58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 59, Sequence 61, Sequence 61, Sequence 61, Sequence 10, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 12, Sequence 139, Sequence 39, Sequ
                                                                                                                                                           US-09-996-617-8_COPY_111_181
378
1 GLHFIDQHRAALIARVTNVE......LFSFTPAWNWTCKDLLLQAL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-340-620A-58
US-09-340-620A-59
US-09-340-620A-69
US-09-340-620A-61
US-09-340-620A-71
US-09-340-620A-71
US-09-069-023-8
US-09-069-023-8
US-09-069-023-8
US-09-069-033-8
US-09-245-281-31
US-09-245-281-31
US-09-245-281-31
US-09-340-620A-10
US-09-340-620A-10
US-09-340-620A-10
US-09-340-620A-10
US-09-340-620A-10
US-09-245-281-41
US-09-245-281-39
US-09-245-281-39
US-09-245-281-39
US-09-245-281-39
US-09-245-281-39
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                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                           389414 segs, 51625971 residues
GenCore version
Copyright (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                    Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length DB
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Perfect score:
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Maximum DB seq
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                                                              OM protein
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| Sequence 58, Application US/09340620A |
| Sequence 58, Application US/09340620A |
| Patent No. 648293 |
| GENERAL INFORMATION: |
| APPLICATION SETTING THE CARD-RELATED PROTEIN FAMILY AND USES THER TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THER FILE REFERENCE: 07344-12401 |
| TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THER CURRENT FILING DATE: 1999-06-28 |
| PRIOR FILING DATE: 1999-02-05 |
| PRIOR FILING DATE: 1998-06-17 |
| PRIOR FILING DATE: 1998-06-17 |
| PRIOR FILING DATE: 1998-06-17 |
| PRIOR FILING DATE: 1998-06-17 |
| PRIOR FILING DATE: 1998-06-17 |
| PRIOR FILING DATE: 1998-06-17 |
| PRIOR FILING DATE: 1998-06-17 |
| ROFFWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 58 |
| LENGTH: 71 |
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US-09-340-620A-49
US-09-340-620A-49
Sequence 49, Application US/09340620A
Patent No. 6482933
GENERAL INFORMATION:
TAPLICANT: BETEIN FAMILY AND USES THER
PILE REFERENCE: 07334-124001
PILE REFERENCE: 07334-124001
CURRENT APPLICATION NUMBER: US/09/340,620A
CURRENT FILING DATE: 1999-06-28
PRIOR APPLICATION NUMBER: US 09/245,281
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100.0%; Score 378; DB 4; Length 7
Best Local Similarity 100.0%; Pred. No. 1.5e-42;
Matches 71; Conservative 0; Mismatches 0; Indels
US-09-207-359B-46
US-09-865-364-46
US-09-245-2811-8
US-09-207-359B-8
US-09-340-620A-8
US-09-340-620A-6
US-09-340-620A-6
US-09-340-620A-6
US-09-340-620A-6
US-09-360-033-5
US-09-069-023-5
US-09-069-023-5
US-09-069-023-5
US-09-069-023-5
US-09-069-023-1
US-09-069-023-1
US-09-069-023-1
US-09-069-023-1
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GENERAL INFORMATION:

### SEQUENCE 61, Application US/09340620A

### SEQUENCE 61, Application US/09340620A

### SEQUENCE 61, Application US/09340620A

### SEQUENCE No. 6482933

### GENERAL INFORMATION:

### SEPLICATION:

### SECOLOR OF INFORMATION:

### TITLE OF INFORMATION:

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IITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
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Pred. No. 1.6e-27;
7; Mismatches 11; Indels
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                           FILER REFERENCE: 107344-124001
CURRENT APPLICATION NUMBER: US/09/340,620A
CURRENT FILING DATE: 1999-06-28
PRIOR APPLICATION NUMBER: US 09/245,281
PRIOR PILING DATE: 1999-02-05
PRIOR PILING DATE: 1998-12-08
PRIOR PILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PSECSE FOR WINDOWS VERSION 4.0
SOFTWARE: PSECSE FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 69.8%;
I Similarity 73.9%;
51; Conservative '
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Matches 51, Conservative
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-340-620A-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-340-620A-66
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Best Local Similarity
Matches 51; Conserv
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Sequence 57, Application US/09340620A

Patent No. 648233

GENERAL INFORMATION

APPLICANT: Bestin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE: 07344-124001

CURRENT APPLICATION NUMBER: US/09/340,620A

CURRENT PILING DATE: 1999-06-28

PRIOR APPLICATION NUMBER: US 09/245,281

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

NUMBER OF SEQ ID NOS: 71

LENGTH: 70

LENGTH: 70
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   PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: US 09/207,359
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/019,041
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-02-06
NUMBER OF SEQ. ID NOS: 71
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 49
LENGTH: 195
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US-09-340-620A-66
Sequence 66, Application US/09340620A
; Patent No. 6482933
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Matches 51; Conservative
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                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Mus musculus
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APPLICANT: Bertin, John
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US-09-340-620A-57
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Sequence 22, Application US/09069023A

Sequence 22, Application US/09069023A

Sequence 22, Application US/09069023A

GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Nunez, Gabriel
APPLICANT: Nonez, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
TITLE REFERENCE: UW-03333
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT PILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SOUTHARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 221
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APPLICANT: Nunez, Gabriel
APPLICANT: Inhobara, Nachiro
APPLICANT: Inhobara, Takeyoshi
TAPLICANT: Inhobara, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: GIGALLING PATHWAY INHIBITORS AND ACTIVATORS
FILE REPERENCE: UM-0333
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SCOTTWARE: PATENTIN Ver. 2.0
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18.4%; Score 69.5; DB 4; Length 221;
Best Local Similarity 26.8%; Pred. No. 0.3;
Matches 22; Conservative 12; Mismatches 23; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;; Score 69.5; DB 4;
;; Pred. No. 0.28;
12; Mismatches 23;
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72 ACQELLRCAQQTVSMPDPAWDW 93
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|||:|
72 ACQELLRCAQRTAGAPDPAWDW 93
                                                                                                                                                            ; Sequence 8, Application US/09069023A; Patent No. 6348573
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Best Local Similarity 26.8%;
Matches 22; Conservative 12
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ORGANISM: Homo sapiens
US-09-069-023-8
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US-09-069-023-22
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US-09-069-023-22
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                       Sequence 71, Application US/09340620A

Patent No. 648293
GENERAL INFORMATION
APPLICANT: Beatin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE: 07334-124001
CURRENT APPLICATION NUMBER: US/09/340,620A
CURRENT FILING DATE: 1999-02-06-28
PRIOR APPLICATION NUMBER: US 09/245,281
PRIOR APPLICATION NUMBER: US 09/245,281
PRIOR PELING DATE: 1998-12-08
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-02-06
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL Machino
APPLICANT: Inchara, Machino
APPLICANT: Acseki, Takeyoshi
TITLE OF INVENTION: CONFOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REPERENCE: UM-03333
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTIN VET. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEATURE:
OTHER INFORMATION: Consensus sequence
NAME/KEY: VARIANT
LOCATION: (1) ... (109)
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/09069023A Patent No. 6348573
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 22; Conserv
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LENGTH: 106
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Patent No. 6369196
GENERAL INFORMATION:
APPLICANT: Bertin.
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION WOWER: US/09/245,281
CURRENT APPLICATION NUMBER: US/09/245,281
CURRENT FILING DATE: 1999-02-05
EARLIER FILING DATE: 1999-102-05
EARLIER FILING DATE: 1998-102-06
EARLIER PILING DATE: 1998-102-06
EARLIER PILING DATE: 1998-102-06
EARLIER PILING DATE: 1998-06-17
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EARLIER PILING DATE: 1998-06-17
EARLIER PILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 44
EARLIER PILING DATE: 1998-02-06
SEQ ID NO 31
EARLIER PILING DATE: 1998-02-06
SEQ ID NO 31
EARLIER PILING DATE: 1998-02-06
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Sequence 31, Application US/09099041A

Sequence 31, Application US/09099041A

Patent No. 6346576

GENERAL INFORMATION:

TILLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

TILLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: 07334-076001

CURRENT APPLICATION NUMBER: US/09/099,041A

CURRENT FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 37

SEQ ID NO 31

LENGTH: 94
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25.9%; Pred. No. 0.34;
tive 12; Mismatches 23;
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US-09-099-041A-31
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Best Local Similarity
Matches 21; Conservat
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RESULT 12 US-09-207-359B-31

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VS-09-430-620A-31

VS-09-430-620A-31

Sequence 31, Application US/09340620A

Patent No. 6482933

GENERAL INCORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE

FILE REFERENCE: 07344-124001

CURRENT APPLICATION NUMBER: US/09/340,620A

CURRENT APPLICATION NUMBER: US 09/245,281

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1998-12-08

PRIOR FILING DATE: 1998-12-08

PRIOR PELLOR OWNERS: US 09/207,359

PRIOR PELLOR DATE: 1998-06-17

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Sequence 31, Application US/09207359B
Patent No. 6465140
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVER: US/09/207,359B
CURRENT PILING DATE: 1998-12-08
FRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 47
SOFTWARE: RattsEQ for Windows Version 4.0
SEQ ID NO 31
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Patent No. 6340576

GENERAL INFORMATION:
APPLICANT BETTIN. JOHN

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
CURRENT APPLICATION NUMBER: US/09/099,041A
CURRENT FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENOTH: 100
TYPE: PRT

TYPE: PRT

TYPE: PRT

TYPE: PRT
                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
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Sequence 31, Application US/09865364 Patent No. 6613521
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Best Local Similarity 28.6%
Matches 16; Conservative
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US-09-865-364-31
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-09-099-041A-10
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Search completed: July 28, 2004, 08:55:58 Job time : 12.4036 secs

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July 28, 2004, 08:54:53; Search time 34.6446 Seconds (without alignments) 642.856 Million cell updates/sec
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2: /cgn2_6/ptodata/1/pubpaa/PCT MRW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_NBW PUB.pep:*
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5: /cgn2_6/ptodata/1/pubpaa/USO6_NBW PUB.pep:*
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7/cgn2_6/ptodata/1/pubpaa/USO8_NBW PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_NBW PUB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seg length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 58, Appl Sequence 58, Appl Sequence 8, Appli	Sequence o, Applia Sequence 7, Appli Sequence 49, Appl Sequence 8, Applia	ָ מיע מיע	Sequence 84, Appl Sequence 5, Appli Sequence 5421, Ap Sequence 15, Appl
SUMMARIES	US-09-728-721-58 US-10-295-981-58 US-09-841-8798-8	US-10-756-097-8 US-09-931-071-7 US-09-728-721-49 US-09-96-617-8	US-09-841-8/9E-5 US-10-446-046-4 US-10-295-981-49 US-10-240-145-55	US-10-131-410-84 US-10-756-097-5 US-10-106-698-5421 · US-09-841-879B-15
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16 US-10-756-09	9 US-09-728	9	14 US-10-295-981	14 US-10-295-981	9 US-09-841-879E	16	9 US-09-728-721-6	9 US-09-841-879B	14 US-10-295-981-	16 US-10-756-09	D 6	14	12 10 US-09-895-298-139	σ	თ		12	H	14	14	14	29 14 US-10-183-770-3	14	60-SD 6	9	12 US-1	14 US-10-106-698-5	90 9 US-09-925-301-1120	55 10 US-09-895-298-145
71.2	8.69	69.8	8.69	8.89	69.8	69.8	264 69.8 193	8.69	69.8	69.8	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57,1	57.1	216 57.1 1429	57.1	57.1	57.1	7.1	57.1	57.1	56.6	vo	1 37.3
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ALIGNMENTS

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US-09-728-721-58

US-09-728-721-58

Sequence 58, Application US/09728721

Patent No. US20020061845A1

GENERAL INFORMATION:

GENERAL INFORMATION:

PATENT SETTING OF THE CARD-RELATED PROTEIN FAMILY AND USES THER FILE OF INVENTION: NOVEL WOLSCULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THER FILE OF INVENTION: NOVEL WORDS: US/09/728,721

CURRENT FFLICATION NUMBER: US/09/728,721

CURRENT PELICATION NUMBER: US/09/728,721

CURRENT PELICATION NUMBER: US/09/09,041

PRIOR FILING DATE: 1998-12-08

PRIOR APPLICATION NUMBER: US/09/09,041

PRIOR APPLICATION NUMBER: US/09/09,041

PRIOR APPLICATION NUMBER: US/09/019,942

PRIOR APPLICATION NUMBER: US/09/019,942

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PRIOR APPLICATION NUMBER: US/09/019,942

PRIOR APPLICATION NUMBER: US/09/019,942

PRIOR APPLICATION NUMBER: US/09/019,942

PRIOR APPLICATION NUMBER: US/09/01
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Sequence 8, Application US/10756097

Sequence 8, Application US/10756097

Publication No. US20040127685A1

GENERAL INFORMATION: USEOUGH MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND TITLE OF INVENTION: USES THEREOF

FILE REPRENCE: 07334-330001

CURRENT PILING DATE: 2004-01-13

PRIOR APPLICATION NUMBER: US/09/841,879B

PRIOR APPLICATION NUMBER: US/09/841,879B

PRIOR APPLICATION NUMBER: US 09/728,721

PRIOR APPLICATION NUMBER: US 09/328,721

PRIOR PAPLICATION NUMBER: US 09/328,721

PRIOR PELING DATE: 2000-12-01

PRIOR FILING DATE: 1999-06-28

NUMBER OF SEQ ID NOS: 19

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 85
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APPLICANT: Alnemti, Emad S.
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN PAMILY AND USES THEREOF
FILE REFERENCE: 07334-335001
CURRENT APPLICATION NUMBER: US/09/931,071
CURRENT FILING DATE: 1999-10-27
PRIOR PELLING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 378; DB 16;
; Pred. No. 6.9e-40;
0; Mismatches 0;
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Sequence 7, Application US/09931071
Patent No. US20020128219A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 71; Conservative 0;
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61 WTCKDLLLQAL 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; ORGANISM: Homo sapiens
US-10-756-097-8
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US-09-931-071-7
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Matches 71; Conserv
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                                        USECULO 295-981-58

Sequence 58, Application US/10295981

Sequence 58, Application US/10295981

Sequence 58, Application US/20030120055A1

Sequence 58, Application

MORENT NO. US20030120055A1

APPLICANT: Bertin, John

TITLE OF INFORMATION:

CURRENT FILIS DATE: 2003-11-15

CURRENT FILING DATE: 1099-06-28

PRIOR PELION NUMBER: US/09/340,620

PRIOR PELION NUMBER: US 09/245,281

PRIOR APPLICATION NUMBER: US 09/245,281

PRIOR PELING DATE: 1999-02-05

PRIOR PELING DATE: 1998-06-17

PRIOR PELING DATE: 1998-06-17

PRIOR PELING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR PELING DATE: 1998-06-17

PRIOR PELING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: US 09/099,041

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: US 09/019,942

PRIOR APPLICATION NUMBER: US 09/019,942

PRIOR APPLICATION NUMBER: US 09/019,942

PRIOR APPLICATION NUMBER: US 09/019,942

NUMBER OF SEQ ID NOS: 71

SOFTWARE: FREESEQ for Windows Version 4.0

SEG ID NO 58
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US-09-441-879B-8

PAPPLICATION US/09841879B

PATENT NO. US20020142979A1

GENERAL INFORMATION:

APPLICANT: Bertin, John

TILLE OF INVENTION: NOVEL WOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE: 07334-33001

CURRENT APPLICATION NUMBER: US/09/841,879B

CURRENT FILING DATE: 2001-04-24

PRIOR APPLICATION NUMBER: US 09/728,721

PRIOR APPLICATION NUMBER: US 09/728,721

PRIOR APPLICATION NUMBER: US 09/340,620

PRIOR FILING DATE: 1999-06-28

NUMBER OF SEQ ID NOS: 19

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8
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; ORGANISM: Homo sapiens
US-10-295-981-58
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 71; Conserv
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Sequence 5, Application US/09841879B
Sequence 5, Application US/09841879B
Patent No. US20020142979A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THER.
FILE REPRENCE: 0734-33001.
FILE REPRENCE: 0734-33001.
FILE REPRENCE: 0734-33001.
FRIOR REPLICATION NUMBER: US/09/841,879B
CURRENT FILING DATE: 2001-04-24
RIOR APPLICATION NUMBER: US 09/728,721
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 1999-06-28
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| Publication No. US20030224438A1
| GENERAL INPORMATION:
| APPLICAMY: Berlin, John
| APPLICAMY: Berlin, John
| APPLICAMY: Millennium Pharmaceuticals, Inc.
| TITLE OF INVENTION: NOVEL WOLECULES OF THE PYRIN/NBS/LRR;
| TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF;
| TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF;
| CURRENT FILMO DATE: 2003-05-23
| PRIOR APPLICATION NUMBER: 60/383487
| PRIOR FILMO DATE: 2002-05-24
| NUMBER OF SEQ ID NOS: 5
| SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 195
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
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Best Local Similarity
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LENGTH: 195
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                                                                                                                                             Patent No. US20020061845A1

Patent No. US20020061845A1

GENERAL INFORMATION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE TTILE OF INVERNATION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE CURRENT FILING DATE: 2000-12-01

PRIOR FILING DATE: 1999-06-28

PRIOR APPLICATION NUMBER: US 09/207, 359

PRIOR APPLICATION NUMBER: US 09/207, 359

PRIOR APPLICATION NUMBER: US 09/207, 359

PRIOR APPLICATION NUMBER: US 09/099,041

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-20

PRIOR APPLICATION NUMBER: US 09/019,942
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100.0%; Score 378; DB 9; Length 195;
Best Local Similarity 100.0%; Pred. No. 1.8e-39;
Matches 71; Conservative 0; Mismatches 0; Indels 0
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Sequence 8, Application US/0996617

Sequence 10. US20020128198A1

SEXEMINAL INFORMATION.

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

TITLE OF INVENTION: NOVER: US/09/996,617

CURRENT FILING DATE: 2001-08-15

PRIOR PRICATION NUMBER: 09/931,071

PRIOR FILING DATE: 1999-10-27

PRIOR FILING DATE: 1999-06-28

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 8

LENTH: 195

LENTH: 195
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 49
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Best Local Similarity luv...
Local 71; Conservative
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61 WTCKDLLLQAL 71
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US-09-996-617-8
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111 GLHFIDQHRAALIARVTNVEWLLDALYGKVLTDEQYQAVRAEPTNPSKWRKLFSFTPAWN 170
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APPLICANT: SCHMITT, ARMIN
APPLICANT: SCHMITT, ARMIN
APPLICANT: SCHMITT, ARMIN
APPLICANT: SCHMITT, ARMIN
APPLICANT: BULAKSKY, CHRISTIAN
APPLICANT: ROSENTHAL, ANDRE
TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST
TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST
TITLE OF INVENTION: TUMORS
FILE REFERENCE: SCH-1763
CURRENT APPLICATION NUMBER: US/10/131,410
CURRENT FILING DATE: 2000-09-20
PRIOR PELICATION NUMBER: 09/646,673
PRIOR FILING DATE: 1999-03-19
PRIOR PLING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 202
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 84
LENGTH: 195
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Publication No. US20040127685A1
GENERAL INFORMATION: NO US20040127685A1
GENERAL INFORMATION: USE
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 07334-330001
CUTRENT FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: US/10/756,097
CUTRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: US/09/841,879B
PRIOR APPLICATION NUMBER: US 09/728,721
PRIOR APPLICATION NUMBER: US 09/340,620
                                                                                                                                                                                                                                      1 GLHFIDQHRAALIARVTNVEWLLDALYGKVLTDEQYQAVRAEPTNPSKMRKLFSFTPAWN
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                                                                                                                    Length 195;
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                                                                                                          Query Match
100.0%; Score 378; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.8e-39;
Matches 71; Conservative 0; Mismatches 0;
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100.0%; Score 378; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.8e-39;
Matches 71; Conservative 0; Mismatches 0;
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Sequence 84, Application US/10131410
Publication No. US20030235915A1
GENERAL INFORMATION:
APPLICANT: SPECHT, THOMAS
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                ; ORGANISM: Homo sapiens
US-10-240-145-55
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                           ## Sequence 49, Application US/10295981

| Sequence 49, Application US/10295981
| Publication No. US2030120055A1
| GENERAL INFORMATION:
| APPLICANT: Bertin, John
| TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
| FILE REFERENCE: 0734-124001
| CURRENT APPLICATION NUMBER: US/09/340,620
| PRIOR APPLICATION NUMBER: US/09/340,620
| PRIOR PLING DATE: 1999-06-28
| PRIOR FILING DATE: 1999-06-26
| PRIOR PLING DATE: 1999-06-06
| PRIOR APPLICATION NUMBER: US/09/207,359
| PRIOR PLING DATE: 1999-06-17
| PRIOR APPLICATION NUMBER: US/09/09,041
| PRIOR APPLICATION NUMBER: US/09/019,942
| PRIOR FILING DATE: 1998-06-17
| PRIOR FILING DATE: 1998-06-17
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CURRENT APPLICATION NUMBER: US/10/240,145
CURRENT PILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: 09/640,27
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/68,680
PRIOR PLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 09/695,618
PRIOR FILING DATE: 2000-10-33
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ IN NOS: 172
SSOFFWARE: CUSCOM
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100.0%; Pred. No. 1.8e-39;
ive 0; Mismatches 0;
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US-10-240-145-55
; Sequence 55, Application US/10240145
; Publication No. US20030235883A1
; GENERAL INFORMATION:
                                                  171 WTCKDLLLQAL 181
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Best Local Similarity 100.
Matches 71; Conservative
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   61 WTCKDLLLQAL
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1 GXHFXDQHRAALIARVTXVXXVLDALYGXVLTEXQYQAVRAETTXXXXKYRKLFSFXPSWN 60
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US-09-841-879B-15
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NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 85
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                                                                                                                                                               OTHER INFORMATION: Consensus sequence
                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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Publication No. US20030109690A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Colon and Colon Cancer Associated Polymucleotides and Polypeptide
FILE REFERENCE: PADOSE1
CURRENT FILING DATE: 2002-03-27
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1090-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-11-03
WUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE: 0734-33001
CURRENT APPLICATION NUMBER: US/09/841,879B
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: US 09/728,721
PRIOR APPLICATION NUMBER: US 09/340,620
PRIOR FILING DATE: US 09/340,620
PRIOR FILING DATE: US 09/340,620
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100.0%; Score 378; DB 14; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.9e-39;
Matches 71; Conservative 0; Mismatches 0; Indels 0
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PRIOR FILING DATE: 1999-06-28
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/09841879B Patent No. US20020142979A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           171 WTCKDLLLQAL 181
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                                                                                                               TYPE: PRT
CORGANISM: Homo sapiens
US-10-756-097-5
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US-10-106-698-5421
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OM protein - protein search, using sw model

July 28, 2004, 08:50:22 ; Search time 10.2651 Seconds (without alignments) 665.325 Million cell updates/sec Run on:

US-09-996-617-8_COPY_111_181 378 1 GLHFIDQHRAALIARVTNVE......LFSFTPAMNWTCKDLLLQAL 71

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 Total number of hits satisfying chosen parameters:

283366 segs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: Dir1:*
2: Dir2:*
3: Dir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	hypothetical prote	/prc	hypothetical prote	hypothetical prote	cytochrome-c perox	끍	alpha-glucosidase	hypothetical prote	translation elonga	cal	hypothetical prote	probable lipoate-p	mar	probable outer mem	hypothetical prote	glucan endo-1,3-be	conserved hypothet	hypothetical prote	beta-lactamase (EC	arylamine N-acetyl	spermidine/putresc	major outer membra	protein R07E5.3 [i	log R	A-alpha X protein	probable ABC trans	gal	hetical	27F
		QI.	T17255	870009	A87136 .	T04197	G81417	S57940	AE2402	T21132	A48470	T21133	F83616	AF0294	T17608	H82011	C71274	JN0772	C83295	T39513	52	I58425	22	æ	œ	843599	627	D70873	7094	O	9650
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		Score	216	69.5	89	64.5	64	62.5	62	ä	61.5	ä	61	61	61	o.	60.5	ö	60	9	59.5	6	59	59	59	59	59	59	59	59	29
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# 7 7	L-xylulokinase (EC gag polyprotein - metallopeptidase X	transcription regumajor outer membra	hypothetical proce hypothetical proce arylamine N-acetyl GDF-1 embryonic gr	hypothetical prote translation elonga heta-1 3-clucanase	H+-exporting ATPas
B61267 T04861 C75143	AD0978 S46346 B82788	A12271 S68069	AG5575 F70943 I67465 B39364	T29544 S16308	S62063
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290 368 443	498 554 700	371	0000 0000 0000 0000	380 446	233
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58.88 58.50 50.50	588.5 88.5 58.55	, 55 S		57.5	57
30 31 32	3 3 3 5 4 5 5 4 5	3.6	2 6 4 4 2 9 0 1	44	4. 4. 4. 7.

RESULT 1
17255
hypothetical protein DKFZp58601822.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17255
R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber 1999
A;Accession: T17255
A;Accession: T17255
A;Scatus: preliminary
A;Molecule type: mRNA
A;Residues: 1-1192 < KOB3A;Cross-references: EMBi:All17470
A;Experimental source: adult uterus; clone DKFZp58601822
C;Genetics:
A;Note: DKFZp58601822.1

Gaps ; 0 Query Match 57.1%; Score 216; DB 2; Length 1192; Best Local Similarity 61.4%; Pred. No. 6.1e-17; Matches 43; Conservative 12; Mismatches 15; Indels

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62 TCKDLLLQAL 71 à g

1158 KCKDGLYQAL 1167

RESULT 2
\$70009
glutamate/proline-rich protein (clone 53.1.1.1) - rat
glutamate/proline-rich protein (clone 53.1.1.1) - rat
glutamate/proline-rich protein (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
R;Geettman, R.; McMahon, A.; Sabban, E.L.
Biochim. Biophys. Acta 1306, 147-152, 1996
A;Title: Cloning and characterization of cDNAs for novel proteins with glutamic acid-pr
A;Reference number: \$70009; MUID:96221285; PMID:8634331
A;Reference number: \$70009
A;Retus: preliminary
A;Molecule type: mRNA
A;Residues: 1-221 cGEE>
A;Cross-references: EMBL:U40627; NID:gl184693; PIDN:AAB05667.1; PID:gl184694

Gaps 25; Length 221; Ouery Match 18.4%; Score 69.5; DB 2; Length 22 Best Local Similarity 26.8%; Pred. No. 1.3; Matches 22; Conservative 12; Mismatches 23; Indels

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5 IDQHRAALIARV-TNVEWLLDALYGK-VLTDEQYQAVRAEPTNPSKMRKLFSFT----- 56

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Cipate: 31-Mar-2000 #text_change 03-Jun-2002
Cipate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
Cipacession: GB1417
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyg.
A;Reference number: A01250; MUID:20150912; PMID:10688204
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Cross-references: GB:AL1139074; GB:AL111168; NID:g6967505; PIDN:CAB72513.1; PID:g696752
A.Experimental source: serotype O2, strain NCTC 11168
                                                           cytochrome-c peroxidase (EC 1.11.1.5) Cj0020c [similarity] - Campylobacter jejuni (strai
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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AB2402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 GSQFAEELRSAFAAVAMLASLVWFYSLAFGAVVLSPWLARSR---QGYSKLLILLLVSPC 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Systa protein homolog - Aeromonas hydrophila
C;Species: Aeromonas hydrophila
C;Species: Aeromonas hydrophila
C;Species: Aeromonas hydrophila
C;Species: Aeromonas hydrophila
C;Species: Aeromonas hydrophila
C;Species: Serial: 1201-1996 #sequence_revision 01-Mar-1996 #text_change 08-Oct-1999
C;Accession: S57940
B;Swift, S.; Fish, L.; Williams, P.; Stewart, G.S.A.B.
A;Reference number: S57938
A;Reference number: S57938
A;Reference number: S57940
A;Accession: S57940
A;Status: preliminary
A;Accession: S57940
A;Status: preliminary
A;References: EMBL:X89469; NID:g899143; PIDN:CAA61655.1; PID:g899146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.5%; Score 62.5; DB 2; Length 2 24.6%; Pred. No. 8.3; indels ive 11; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Indels
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16.9%; Score 64; DB 2
Best Local Similarity 29.0%; Pred. No. 8.4;
Matches 20; Conservative 7; Mismatches
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Best Local Similarity 24.6%
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 TCKDLLLQA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA A; Residues: 1-304 < PAR>
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C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
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C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: ST; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hc
R; Davies, R.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1077-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Accession: A87136
A;Accession: A87136
A;Accession: A87136
A;Accession: A87136
A;Cossion: A87136
A;C
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C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Acate: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 28-Jul-2000
C.Accession: T04197
R.Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.
Submitted to the Protein Sequence Database, March 1999
A.Reference number: Z15260
A.Reference number: Z15260
A.Residues: 1-605 - ABEV>
A.Residues: 1-605 - ABEV>
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18.0%; Score 68; DB 2
Best Local Similarity 36.4%; Pred. No. 5.5;
Matches 20; Conservative 3; Mismatches
                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                     72 ACQELLRCAQQTVSMPDPAWDW 93
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Matches 22
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RESULT 5

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hypothetical protein PA0234 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83616
R;Accession: F83616
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Badman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim invarve, Acc, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path A;Accession: F83616
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A;Status: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: GB:AE004461; GB:AE004091; NID:g9946066; PIDN:AAG03623.1; GSPDB:GN00
A;Cross-references: GB:AE004461; GB:AE004091; NID:g9946066; PIDN:AAG03623.1; GSPDB:GN00
C;Genetics:
A;Gene: PA0234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 4
A;Introns: 18/1; 74/3; 135/1; 222/3; 258/3; 279/1; 379/1; 496/1; 791/2; 867/1; 969/1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1193 «ML->
A;Cross-references: EMBL:569636; PIDN:CAA93465.1; GSPDB:GN00022; CESP:F20B10.1
A;Experimental source: clone F20B10
                                                                    346 VDCHTAHIACKFAVLEKRLDRRSGRALEDDPKFIKTGDAAIIKMEPSKPMCVESFIEYPP 305
                                                                                                                                                                                                                                                                                                              T21133
hypothetical protein F20B10.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Dacession: T21133
R;Percy, C.
                                --- OYQAVRAEPTNPSKMRKLFSFTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 QHRAALIARV-----TNVEWLLDAL---YGKVLTDEQYQAVRAEPTNPSKM-RKLFSFTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, February 1996 A;Reference number: Z19380 A;Accession: T21133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
16.3%; Score 61.5; Di
Best Local Similarity 34.0%; Pred. No. 76;
Matches 17; Conservative 10; Mismatches
                                5 IDOHRAALIARVTNVEWLLDALYGKVLTDE----
                                                                                                                                                                                                     LGRFAVRDM 314
                                                                                                                                               58 AWNWTCKDL
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.D.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Rtes. 9, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUD:21595285; PMID:11759840
A;Accession: RE2402
A;Status: preliminary
A;Molecule type: DNA
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C,Species: Eimeria bovis
C,Bate: 01-bec-1993 #sequence_revision 15-oct-1994 #text_change 12-Apr-1995
C,Accession: A48470
R,Abrahamsen, M.S.; Clark, T.G.; Mascolo, P.; Speer, C.A.; White, M.W.
MOI. Blochem. Parasitol. 57, 1-14, 1993
A,Title: Developmental gene expression in Eimeria bovis.
A,Reference number: A48470; MUID:93149194; PMID:8426605
A,Accession: A48470
A,Molecule type: mBNA
A,Molecule type: mBNA
A,Molecule type: mBNA
A,Residues: 1-346 cABR>
A,Experimental source: merozoites
A,Note: sequence extracted from NCBI backbone (NCBIN:123619, NCBIP:123622)
C,Superfamily: translation elongation factor Tu; translation elongation factor Tu PC; Keywords: GTP binding; protein blosynthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F20B10.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21132
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                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 779;
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A;Reference number: 219380
A;Accession: T22132
A;Accession: T22132
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Cross-references: BMBL:269636, PIDN:CAA93464.1;
A;Cross-references: BMBL:269636, PIDN:CAA93464.1;
C;Genetics:
A;Gene: CESP:PP08110.2
A;Agene: CESP:PP08110.2
A;Apap position: 4
A;Introns: 18/1; 74/3; 135/1; 222/3; 258/3; 279/1
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16.3%; Score 61.5; DB
Best Local Similarity 21.7%; Pred. No. 19;
Matches 15; Conservative 13; Mismatches
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16.3%; Score 61.5; DE
Best Local Similarity 34.0%; Pred. No. 17;
Matches 17; Conservative 10; Mismatches
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Best Local Similarity 35.7%; Pred. No. 41;
Matches 15; Conservative 6; Mismatches
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57 56

> Gaps 7 ;

34; Indels

Gaps

17;

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C;Accession: H82011
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel; Holroy, S.; Jagells, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUD:20222556; PMID:10761919
A;Accession: H82011
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-464 <PAR>
A;Residues: 1-464 <PAR>
A;Cross-references: GB:AL162752; GB:AL157959; NID:G7378778; PIDN:CAB83493.1; PID:G737895
A;Genetics:
A;Genetics:
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C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 24-Nov-1999
C;Accession: C71274
C;Accession: C71274
R;Fraser, CM.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDd they, D.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
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A;Cross-references: GB:AE001255; GB:AE000520; NID:g3323156; PIDN:AAC65821.1; PID:g332316
A;Experimental source: strain Nichols
C;Genetics:
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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16.0%; Score 60.5; DB 2; Length 72
Best Local Similarity 26.9%; Pred. No. 57;
Matches 21; Conservative 17; Mismatches 27; Indels
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C;Superfamily: syphilis spirochete hypothetical protein TP0851
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Job time : 12.2651 secs
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Best Local S
Matches 18
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                                                                                                                 probable lipoate-protein ligase A lplA [imported] - Yersinia pestis (strain C092)
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Species: O2-Nov-2001
C;Accession: AF00294
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Accession: AF0294
A;Accession: AF0294
A;Accession: AF0294
A;Residues: 1-338 <KUR>
A;Residues: 1-338 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC91218.1; PID:g15980407; GSPDB:GN00175
C;Genetics:
A;Genetics:
A;
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M2011.
probable outer membrane protein NMA0178 [imported] - Neisseria meningitidis (strain Z249
C,Species: Neisseria meningitidis
C,Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pirobable GDPmannose 4,6-dehydratase (EC 4.2.1.47) - Chlorella virus PBCV-1 N,Alternate names: GDP-D-mannose dehydratase C.$Becies: Chlorella virus PBCV-1 C.$Becies: Chlorella virus PBCV-1 C.$Becies: Chlorella virus PBCV-1 C.$Becies: Chlorella PECV-1 C.$Becies: Chlorella Library, May 1999 C.$Accession: T17608 A.$Reference number: 218806 A.$Reference number: 218806 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Accession: T17608 A.$Acc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --- LYGKVLTDEQYQAVRAEPTNPSK 48
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151 VAKLYAY-----WICKN 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 32.33
Matches 21; Conservative
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Matches 22; Conserv
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Gaps

13;

OM protein - protein search, using sw model

July 28, 2004, 08:46:37 ; Search time 6.84337 Seconds (without alignments) 540.228 Million cell updates/sec Run on:

US-09-996-617-8_COPY_111_181 378 1 GLHFIDQHRAALJARVTNVE......LFSFTPAMNWTCKDLLLQAL 71 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	homod	2	homo	brack		mus n	rattus	hom	mus mu	gal						Q07051 eimeria bov		hom	•		P79784 gallus gall							шns	mus	mus	032723 bacillus sp	ratt	P27545 mus musculu
SUMMARIES	ID		ASC_MOUSE	NALI HUMAN	ASC BRARE	NOL3 HUMAN	NOL3 MOUSE	NOL3_RAT	CAR8_HUMAN	RIK2 MOUSE	BIR CHICK	DX52 MOUSE	CAR4_HUMAN	YGGA AERHY	RIK2_HUMAN	DX52_RAT	EF1A_EIMBO	Y851_TREPA	LP15_HUMAN	LR15_MOUSE	DUSA PSEAE	ENP2_CHICK	BLAB_BACFR	ARY2_RAT	GALE_MOUSE	HSLO_STRP3	OP25_HAEIN	Y2R2_DROME	ARY2 MOUSE	BIR2_MOUSE			닸	LSS1_MOUSE
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P25166 stylonychia P23903 bacillus ci	Q98dk4 rhizobium l P22203 saccharomyc	Q9k120 vibrio chol Q99542 homo sapien	P18440 homo sapien	P18645 rattus norv	P17506 xenopus lae	033250 mycobacteri	094952 homo sapien	000750 homo sapien
EFIA STYLE E13B_BACCI	MASZ RHILO VATE YEAST	YBJF_VIBCH	ARY1 HUMAN	GALE_RAT	EF11 XENLA	YL15 MYCTU	FX21 HUMAN	PK3B_HUMAN
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446 682	721	375 508	290	347	463	609	621	1634
15.2	15.2	15.1	14.9	14.9	14.9	14.9	14.9	14.9
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35	34	8 6 6 6	40	41	42	43	44	45

ALIGNMENTS

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Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Expleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robert S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rochein J.B., Warre M.M., Marra M.A.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Whiting A. Schein J.E., Jones S.J.M., Marra M.A.,

When and mouse CDNA sequences "."

Manna A. Manna M. Sone C. Hen A. Schein J. Stone Full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION, AND SUBSCELLULAR LOCATION.

MEDLINE=20552140; PubMed=11103777;

McConnell B.B., Vertino P.M.;

McConnell B.B., Vertino P.M.;

McConnell B.B., Vertino P.M.;

redistration of a caspase-9-mediated apoptotic pathway by subcellular redistribution of the novel caspase recruitment domain protein TMS1.";

Cancer Res. 60:6243-6247(2000)

-! FUNCTION: Promotes caspase-mediated apoptosis. This proapoptotic activity is mediated predominantly through the activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLUIAR LOCATION: Cytoplasmic. Upstream of caspase activation, a redistribution from the cytoplasm to the aggregates occurs. These appeared as hollow, perinuclear spherical, ball-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9ULZ3-2; Sequence=VSP_004119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q9ULZ3-1; Sequence=Displayed;
     MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB023416; BAA87339.2; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=2
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AF184073; AAG01188.1; AF255794; AAF99665.1; AF310103; AAG30286.1;

EMBL; EMBL; EMBL;

AF184072;

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1 GLHFIDQHRAALIARVTNVEWLLDALYGKVLTDEQYQAVRAEPTNPSKWRKLFSFTPAWN 60
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STRAIN=CS7BL/6J; TISSUE=Pancreas, and Tongue;
STRAIN=CS7BL/6J; TISSUE=Pancreas, and Tongue;
Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Kadota K., Matsuda H.A., Ashburner M., Patalov S., Casavant T.,
Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Masumoto J., Taniguchi S., Nakayama K., Ayukawa K., Sagara J.; "Murine ortholog of ASC, a CARD-containing protein, self-associates and exhibits restricted distribution in developing mouse embryos."; Exp. Cell Res. 262:128-133(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASC_MOUSE STANDARD; PRT; 193 AA.
09EPB4, 09D2W4,
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Apoptosis-associated speck-like protein containing a CARD (mASC)
(PYCARD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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STRAIN=FVB/N; TISSUE=Breast tumor;
Martinon F., Hofmann K., Tschopp J.;
Myoard a PYD and CARD containing molecule.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                              Missing (in isoform 3).
/FIId=VSP 004118.
Missing (in isoform 2).
/FIId=VSP 004119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 378; DB 1;
; Pred. No. 3.3e-37;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                Apoptosis, Anti-oncogene, Alternative splicing.
DOMAIN
                                                                                                            MIN, 666838; ...
GO; GO:0006917; P.induction of apoptosis; TAS.
InterPro; IPRO01315; CARD.
InterPro; IPRO01305; PAAD DAPIN_dom.
Fram; PR02758; PAAD_DAPIN; 1.
PROSITE; PSS0209; CARD; 1.
PROSITE; PSS0824; DAPIN; 1.
AF384665; AAK63850.1; -.
AK000211; BAA91012.1; ALT_FRAME.
BC004470; AAH04470.1; -.
BC013569; AAH13569.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/c; TISSUE=Thymus;
MEDLINE=20580347; PubMed=11139337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 AA; 21627 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 Wrckbilioal 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 WICKDLLLQAL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                            107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                93
                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
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                                    EMBL;
EMBL;
EMBL;
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ASC_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DTTTDDDTTDDDTTDDDTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTDDDTTDDDTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTD
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DOMAIN

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REAUGENCE FROM N.A.

SEQUENCE FROM N.A.

STRUBEZE FROM N.A.

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Shemene C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetcow K.H., Scheefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetcow K.H., Scheefer C.F., Bhat N.K.,

Rabacheron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rabascheron M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Rabascheron M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Rabascheron M.J., WcKernan K.J., Malek J.A., Gubes R.A.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Hichards S. A., McEwan P.J., McKernan K.J., Lu X., Gibbs R.A.,

R. Richards S. A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Hichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Hales S. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Hales J., Hellon E., Ketteman W., Madan A., Rodriques S., Sanchez A.

R. Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Blakesley R.W., Tucchman J.W., Green E.D., Dickson M.C.,

R. Blakesley R.W., Tucchman J.W., Green E.D., Dickson M.C.,

R. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. Generation and initial analysis of more than 15,000 full-length

R. Froc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

L. FUNCTION: Promotes caspase-mediated apoptocasis. This proapoptotic

cartivity is mediated predominantly through the activation of

caspase 9 (By similarity).

L. TISSUE SPECIFICITY: Expressed a poptocasis are distribution from the cytoplasm to the aggregates occurs.

These appeared as hollow, perinuclear spherical, ball-like

L. TISSUE SPECIFICITY: Expressed in small intestine, colon, thymus,

spleen, brain, heart, skeletal muscle, kidney, lung and liver.

L. DEVELOPMENTAL STAGE: Strongly expressed at E9:5 day in the
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake U., Befelli D., Bojunga N., Carrinci P., de Bonaldo M.F., Brownstein M.J., Bult C., Pietcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima U., Mazarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-cka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains 1 DAPIN domain.
-!- SIMILARITY: Contains 1 CARD domain.
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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MGD; MGI:1931465; Asc.
GO; GO:0005829; C:cytosol; IDA.
InterPro; IPR001315; CARD.
InterPro; IPR004020; PAAD DAPIN_dom.
Pfam; PF02758; PAAD_DAPIN; 1.
EMBL, AB032249, BAB16609.1, --
EMBL, AK10104; AAG30287.1; --
EMBL, AK00962, BAB26543.1; --
EMBL, AK01742; BAB25229.1; --
EMBL, AK018682; BAB31341.1; --
EMBL, BC008252; AAH08252.1; --
                                                                                                                                                                                                                                                               Pfam, PF02758; PAAD DAPIN;
PROSITE; PS50209; CARD; 1.
PROSITE; PS50824; DAPIN; 1.
                                                                                                                                                                                                                                                                                                                                                     Apoptosis; Anti-oncogene.
DOMAIN 1 91
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111 HFVDOHROALIARVTEVDGVLDALHGSVLTEGGYQAVRAETTSQDKMRKLFSFVPSWNLT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUB-Erythroleukemia;
MEDLINE-21153743; PubMed-11076957;
Hlaing T., Guo R.-F., Dilley K.A., Loussia J.M., Morrish T.A.,
Shi M.M., Vincerz C., Ward P.A.;
"Molecular cloning and characterization of DEFCAP-L and -S, two
isoforms of a novel member of the mammalian Ced-4 family of apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M.,
Miyajima N., Tanaka A., Kotani H., Nomura W., Ohara O.,
"Prediction of the coding sequences of unidentified human genes. XIII.
The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                        3 HFIDQHRAALIARVTNVEWLLDALYGKVLTDEQYQAVRAEPTNPSKMRKLFSFTPAMNWT
                                                                                                                                                                                                                                                                                                                                                                         NAL1 HUMAN STANDARD;

QGC000; QBRZZ8; QBRZS9; Q9HAV8; Q9UFT4; Q9YZE0;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)

NACHT-, LRR- and PYD-containing protein 2 (Death effector filament-forming ced-4-like apoptosis protein) (Nucleotide-binding domain and caspase recruitment domain) (Caspase recruitment domain) (Caspase recruitment domain) (NaLP1 OR DEFCAP OR NAC OR CARD7 OR XIAA0926.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=21169419; PubMed=11270363;
Bettin J., DiStefano P.S.
"The PYRIN domain: a novel motif found in apoptosis and inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=21148093; PubMed=11250163;
Martinon F., Hofmann K., Tschopp J.;
"The pyrin domain- a possible member of the death domain-fold family implicated in apoptosis and inflammation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4), AND PROTEIN INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A novel enhancer of the Apafl apoptosome involved in cytochrome c-dependent caspase activation and apoptosis."; J. Biol. Chem. 276:9239-9245(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=T-cell;
MEDLINE=21153744; PubMed=11113115;
Chu Z.-L., Pio F., Xie Z., Welsh K., Krajewska M., Krajewski S.,
Godzik A., Reed J.C.;
                                                                         Match
Local Similarity 73.9%; Score 264; DB 1; Length 193;
Local Similarity 73.9%; Pred. No. 7.9e-24;
es 51; Conservative 7; Mismatches 11; Indels
                K -> E (IN REF. 3).
2A4EA40194870B31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [3]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dell Death Differ. 7:1273-1274(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 276:9230-9238(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99246063; PubMed=10231032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 2).
105 193 C
159 159 K
193 AA; 21458 MW;
                                                                                                                                                                                                                                                            171 CKDSLLQAL 179
                                                                                                                                                                                                                                   71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Human)
                                                                                                                                                                                                                                     63 CKDLLLQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                  CONFLICT
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                                                                           Query Match
                                                                                                  Best Loca
Matches
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ATP-binding; Leucine-rich repeat; Repeat;
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1119
1184
1241
1366
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Q919N6;
                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
CONFLICT
SEQUENCE
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CONFLICT
CONFLICT
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VARSPLIC
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                                                         REPEAT
REPEAT
                                                                                                                                                 REPEAT
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                                                                                                     REPEAT
                                                                                                                                    REPEAT
                                              DOMAIN
                                                                                                                                                                  DOMAIN
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ASC BRARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                     SUBDIVIT: Interacts strongly with caspase 2, weakly with caspase 9 and with APAFI in a cytochrome c-inducible way leading to the formation of an apoptosome. This interaction may be ATP-dependent. SUBCELDULAR LOCATION: Cytoplasmic.
ALTERNATIVE PRODUCTS:
                                                                       Kochrer K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S., Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Able to form cytoplasmic structures termed death effector filaments. Enhances APAFI and cytochrome c-dependent activation of pro-caspase-9 and consecutive apoptosis. Seems to bind ATP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 1 DAPIN domain.
SIMILARITY: Contains 1 NACHT domain.
SIMILARITY: Contains 1 CARD domain.
SIMILARITY: Contains 7 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO, GO:0005622; C:intracellular; IC.
GO; GO:0016506; F:apoptosis activator activity; NAS.
GO; GO:0018656; F:aspase activator activity; NAS.
GO; GO:0018999; F:enzyme binding; IPI.
GO; GO:006919; P:enzyme binding; IPI.
GO; GO:006917; P:induction of apoptosis; NAS.
InterPro; IPR001315; CARD.
InterPro; IPR001611; IRR.
                                               SEQUENCE OF 282-1473 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IFRO TOTAL INTERPRO; IPRO TOTAL INTERPRO; IPRO TOTAL IN NACHT NYPASE.

InterPro; IPRO 111; NACHT NYPASE.

InterPro; IPRO 120, PAD DAPIN dom. PFO 100 CO. IRR; 2.

Pfam; PFO 5729; NACHT; 1.

Pfam; PFO 5729; PAD DAPIN; 1.

PRO 115; PS 50 209; CARD; 1.

PROSITE; PS 50 824; DAPIN; 1.

PROSITE; PS 50 837; NACHT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AB023143; BANGOT51.1; --
EMBL, AB023143; BANGOT70.1; --
EMBL, ALLITATO; CAB55945.1; --
PIR; TT7255; T17255.
HSSP; P13489; 1A4Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF298548, AAG15254.1; --
EMBL, AF310105; AAG30288.1; --
EMBL, AF229059; AAK00748.1; --
EMBL, AF229060; AAK00749.1; --
EMBL, AF229061; AAK00750.1; --
      large proteins in vitro.";
                    DNA Res. 6:63-70(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                              liver and muscle.
                                                               TISSUE=Uterus;
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its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LHFIDQHRAALIARVINVEWLLDALYGKVLTDEQYQAVRAEPTNPSKWRKLFSFTPAWNW 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the Buropean Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=20373792; PubMed=10917738;
Inohara N., Nunez G.;
"Genes with homology to mammalian apoptosis regulators identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Apoptosis-associated speck-like protein containing a CARD (PYCARD).
ASC OR ASCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- FUNCTION: Promotes caspase-mediated apoptosis (By similarity).
-i- SUBGELLULAR LOCATION: Cytoplasmic.
-i- SIMILARITY: Contains 1 DAPIN domain.
-i- SIMILARITY: Contains 1 CARD domain.
                                                                                                                                                                                                       Missing (in isoform 3 and isoform 4). /FrId=VSP_004326.
                                                                                                                                                                                                                                           Missing (in isoform 2 and isoform 3).
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.1%; Score 216; DB 1; Length 14 61.4%; Pred. No. 3.1e-17; Live 12; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               438F0DCE45C2562D CRC64;
                                                                                                                                                                                                                                                                                                             (IN REF. 1).
(IN REF. 1).
(IN REF. 1).
(IN REF. 1).
(IN REF. 1).
(IN REF. 1).
(IN REF. 1).
(IN REF. 1).
                                                                                                                                                                                                                                                          /FTId=VSP 004327
K->L: NO EFFECT.
K->S: NO EFFECT.
                                                                                                                                                                 CARD.
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 AA
                                                                                                                                                                                                                                                                                                                 LRR 1.
LRR 3.
LRR 4.
LRR 4.
LRR 5.
LRR 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zebrafish.";
Cell Death Differ. 7:509-510(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA; 165865 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 61.4
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1439 KCKDGLYQAL 1448
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1184
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1463
341
987
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                                                                                                                                                                                                                                                                                 340
340
155
246
782
878
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Alternative splicing.
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00114; CARD; 1.
PROSITE; PS50209; CARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GK; O60936; -
MIM; 605235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mar
Local Sim-
22;
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    not removed. Usage by and for commercial reement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                         2 LHFIDQHRAALIARVTNVEWLLDAL-YGKVLTDEQYQAVRAEPTNPSKWRKLFS--FTPA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Koseki T., Inohara N., Chen S., Nunez G.; "ARC, an inhibitor of apoptosis expressed in skeletal muscle and heart that interacts selectively with caspases."; Proc. Natl. Acad. Sci. U.S.A. 95:5156-5160(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MINIOLINE-22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Strausberg R.L., Feingold E.A., Grouse L.H., Shemmen C.M., Schuler G.D., Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Stapleton M., Soazes M.B., Parmer A.A., Rubin G.M., Hong L., Stapleton M. Soazes M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Garninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McBwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                               NOL3 HUMAN STANDARD, PRT, 219 AA.
060937, 28-FEB-2003 (Rel. 41, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Nucleolar protein 3 (Apoptosis repressor with CARD) (Muscle-enriched cytoplasmic protein) (Myp) (Nucleolar protein of 30 kDa) (Nop30).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB=Cervical carcinoma; MEDLINE=99214168; PubMed=10196175; Stoss O., Schwaiger F.-W., Cooper T.A., Stamm S.; Alternative splicing determines the intracellular localization of novel nuclear protein Nop30 and its interaction with the splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                     4,
                                                                                                                                                                                                       ; Score 106; DB 1; Length 203;
; Pred. No. 3e-05;
13; Mismatches 25; Indels
                                                                                                                                                                                                                                 25; Indels
                                                                                                                                                                    112 203 CARD.
203 AA; 22867 MW; EF457179EB7A78A7 CRC64;
modified and this statement is not removentities requires a license agreement (sor send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2] SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                EMBL, AF231013, AAF66956.1; -.
EFIN, SDB-GENE-000511.-2; ascl.
INTERPRO; IPR001315; CARD.
INTERPRO; IPR004020; PAAD_DAPIN_dom.
PÉGMI, PF02758; PAAD_DAPIN, 1.
PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 274:10951-10962(1999)
                                                                                                                                                         DAPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=98226784; PubMed=9560245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                        28.0%;
                                                                                                                                                                                                                                                                                                                                  177 GN-KGKEVLYDAL 188
                                                                                                                                           Apoptosis; Anti-oncogene.
                                                                                                                                                                                                                                  31; Conservative
                                                                                                                                                                                                                                                                                                           59 WINWTCKDLLLQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Kidney;
                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                    NOL3_HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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CED-
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RAPRRCNPGPRRSQSQSWKLRPLKRLNRSRSQSQSWNPRLK
QNQSRNWSQNRTQSPSPTSRKGTSPK1PEGQSSDRRCPAHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=2; Synonym=Myp;
IsoId=O60936-2; Sequence=VSP_000789;
ISSUE SPECIFICITY: Highly expressed in heart and skeletal muscle.
Detected at low levels in placenta, liver, kidney and pancreas.
SIMILARITY: Contains I CARD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 IDRERKRIVETLQADSGLLLDALLARGVLTGPEYEALDALPDAERRVRRLLLLUVGKGEA
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                                                                                                                                                                                                                                                                                                                                                                                                                 apoptosis.
-!-SUBUNT: Isoform 1 oligomerizes and binds to SFRS9/SRp30C and als interacts with NPM1. Isoform 2 binds caspase-2, caspase-8 and CED 3 and inhibits caspase-8 activity.
-!-SUBCELDULAR LOCATION: Nuclear or cytoplasmic. Isoform 1 is found in nucleoli and nucleoplasm. Isoform 2 is cytoplasmic.
-!-ALTERNATIVE PRODUCTS:
EVent-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Sulterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Forc. Natl. Acad. Sci. U.S.A. 99:1699-16903(2002).

P. FUNCTION: The nuclear isoform (1/Nop30) may be involved in RNA splicing and the cytoplasmic isoform (2/Myp) may inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA splicing; Alternative splicing. CARD.
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/FTId=VSP_000789.
24327 MW; BICCCBI99D4FEE09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=1; Synonyms=Nop30;
IsoId=060936-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------PAWNW 61
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EMBL, AF064600, AAC18594.1; --
EMBL, AF064598, AAC18590.1; --
EMBL, AF064598, AAC18591.1; --
EMBL, AF064294, AAC18591.1; --
EMBL, EC012798, AAC18293.1; --
EMBL, BC012798, AAC12798.1; --
Genew, HGNC.7869, NOL3.
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DOMAIN 4 95
VARSPLIC 96 219
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HUMAN
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RESULT
                                                       В
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                                                                                                                                                                                                                                                                    Carrainest Carrain M. Salvandose tissue;

Surgainest Carrainest Ca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: May be involved in RNA splicing (By similarity).
                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.4%; Score 69.5; DB 1; Length 220; 26.8%; Pred. No. 0.64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24567 MW; A4DCD57C1EB320A2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nucleolar protein 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Mismatches
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                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear protein; mRNA splicing.
DOMAIN 4 95 CARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AK021023; BAB32281.1; -.
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InterPro; IPR001315; CARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 26.89
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00114; CARD; 1.
PROSITE; PS50209; CARD; 1
                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218
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220 AA;
                                                                                                                                                             Mus musculus (Mouse)
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                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity)
                        MOUSE
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    MOUSE
NOL3 MOI
Q9D1X0;
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16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2003 (Rel. 42, Last annotation update)
10-CCT-2003 (Rel. 42, Last annotation update)
Caspase recruitment domain protein 8 (Apoptotic protein NDPP1) (DACAR)
(CARD-inhibitor of NF-kappaB activating ligand) (CARDINAL) (TUCAN).
CARDS OR NDPP1 OR KIAA0955.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- TISSUE SPECIFICITY: Highly expressed in skeletal muscle, heart and
-!- TISSUE SPECIFICITY: Highly expressed in skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 IDQHRAALIARV-TNVEWILDALYGK-VLTDEQYQAVRAEPTNPSKMRKLFSFT-----
                                                                                                                                                                                                             Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                  STRAIN=Sprague-Dawley, TISSUE=Brain, and Pheochromocytoma;
MEDLINE=96221285; PubMed=8634331;
Geertman R., MokMon A., Sabban E.L.;
Geortman R., MokMon A., Sabban E.L.;
Gloring and characterization of cDNAs for novel proteins with
glutamic acid-proline dipeptide tandem repeats.";
Biochim. Biophys. Acra 1306:147-152 (1996).
-i. FUNCTION: May be involved in RNA splicing (By similarity).
-i. SUBUNIT: Interacts with SRp30c, NPMI, CASP2, CASP8 and CED-3 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25;
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24576 MW; A7661C9040B2CD4D CRC64;
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                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nucleolar protein 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 18.4%; Score 69.5; DB Local Similarity 26.8%; Pred. No. 0.64; es 22; Conservative 12; Mismatches
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221 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         medulla.
-!- SIMILARITY: Contains 1 CARD domain.
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PIR; $70009; $570009; S70009; S70009; SWART; SWO0114; CARD; 1.
PROSITE; PS50209; CARD; 1.
Nuclear protein; mRNA splicing.
DOMAIN
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STANDARD;
                                                                                                                                                                                               Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107
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Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang H.; "A novel apopototic protein, NDPP1, containing CARD and BH3 domains."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "CARDINAL, a novel caspase recruitment domain protein, is an inhibitor of multiple NF-kappa B activation pathways."; J. Biol. Chem. 276:44069-44077(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION, AND MUTAGENESIS OF LEU-366.
MEDLINE=22062958; PubMed=12067710;
Stilo R., Leconardi A., Formissono L., Di Jeso B., Vito P., Liguoro D.;
Stilo R., Leconardi A., Formissono L., Di Jeso B., Vito P., Liguoro D.;
TUCAN/CARDINAL and DRAL participate in a common pathway for
modulation of NF-kappaB activation.";
FEBS Lett. 521:165-169(2002).
-!- FUNCTION: Inhibits NF-kappa-B activation. May participate in a
requilatory mechanism that coordinates cellular responses
controlled by NF-kappa-B transcription factor. Involved in the
negative regulation of caspase-1.
-!- SUBUNIT: May form homedimers. Interacts with NEMO and DRAL. Binds
to caspase-1, pseudo-ICE and ICEBERG. Interacts with FNBP3 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERIZATION.
MEDLINE=21402909; PubMed=11408476;
MEDLINE=21402909; PubMed=11408476;
MEDLINE=21402909; PubMed=11408476;
Okada K., Marusawa H., Krajewska M., Matsuzawa S.-I., Kim H.,
Okada K., Torii S., Kitada S., Krajewski S., Welsh K., Pio F.,
Godzik A., Reed J.C.;
"TUCAN, an antiapoptotic caspase-associated recruitment domain family J. Biol. Chem. 276:32220-3229(2001).
                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM LONG).
SEQUENCE FROM N.A. (ISOFORM LONG).
MEDLINE-219956691, PubMed-11821383;
MEDLINE-21956691, PubMed-11821383;
MEXEMBAR M., Srinivasula S.M., Wang L., Poyet J.-L., Geddes B.J.,
DiStefano P.S., Bertin J., Alnemri E.S.;
"CARD-8 protein, a new CARD family member that regulates caspase-1
activation and apoptosis.";
J. Biol. Chem. 277:13952-13958(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM LONG).
MEDINE-21570185; Pubmed-11551959;
BOUCHier-Hayes L., Conroy H., Egan H., Adrain C., Creagh E.M.,
MacFarlane M., Martin S.U.;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guiet C., Vito P.;
"DACAR, a novel CARD-containing protein.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guo J.H., Yu L., Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM LONG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM SHORT)
TISSUE=Kidney;
                                                                                             TISSUE=Brain;
MEDLINE=99246063; PubMed=10231032;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM LONG).
                                                                        SEQUENCE FROM N.A. (ISOFORM LONG).
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Name=Short; IsoId=Q9X2G2-2; Sequence=VSP_000782, VSP_000783;

IsoId=Q9Y2G2-1; Sequence=Displayed;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | | :: | | | | | :: :| | | | 344 GAAFVKENHRQLQARMGDLKGVLDDLQDNEVLTENEKEJVEQEKTRQSKNEALLSMVEKK 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GLHFIDQHRAALIARVTNVEWLLDALY-GKVLTDEQYQAVRAEPTNPSKMRKLFSFTPAW
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STRAIN-CS7BL/6;
MEDLINE=21891093; PubMed=11894097;
Chin A.I., Dempsey P.W., Bruhn K., Miller J.F., Xu Y., Cheng G.;
"Involvement of receptor-interacting protein 2 in innate and adaptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune responses.";
Nature 416:190-194(2002).
-!- FUNCTION. Activates pro-caspase-1 and pro-caspase-8. Potentiates
- CASP-8-mediated apoptoosis. Activates NF-kappaB (By similarity).
-!- CATALYIT ATP + a protein = ADP + a phosphoprotein.
-!- CATALYIT Edids to CFLAR/CLARP and CASP1 via their CARD domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37)
RIPK2.

    -!- TISSUE SPECIFICITY: High expression in lung, ovary, testis and
placenta. Lower expression in heart, kidney and liver. Also
expressed in spleen, lymph node and bone marrow.
    -!- SIMILARITY: Contains 1 CARD domain.

                                                                                                                                                                                                                                                                                                                                                                                     286 ELMLS -> WISSL (in isoform Short).
431 Missing (In isoform Short).
Assing (In isoform Short).

7 FILG=VSP 000782.
366 L->R: INHIBITS HOMODIMER FORMATION.
60 E -> G (IN REF. 5).
326 V -> M (IN REF. 5).
422 L -> P (IN REF. 5).
43 48932 MW; CB54D130807732E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 18.1%; Score 68.5; DB 1; Length 431; Local Similarity 27.8%; Pred. No. 1.7; les 20; Conservative 16; Mismatches 35; Indels
                                                                                                                                                                        539 AA.
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60
326
422
431 AA;
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NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                        287
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P58801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
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SEQUENCE
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RIK2 MOUSE
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SEQUENCE FROM N.A.
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REPEAT
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CONFLICT
CONFLICT
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
REPEAT
DOMAIN
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ÎTA OR IAPI.
Gallus gallus (Chicken).
Etwaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIR_CHICK STANDARD; PRT; 611 AA.
090660; 057319;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Inhibitor of apoptosis protein (IAP) (Inhibitor of T cell apoptosis protein).
Binds to BIRC3/c-IAP1 and BIRC2/c-IAP2, TRAF1, TRAF2 and TRAF5 and TRAF6. May be a component of both the TWFRSF1A and TWFRSF5/CD40 receptor complex (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
FTM: Autophosphorylated (By similarity).
STMILARITY: Belongs to the Ser/Thr family of protein kinases.
SIMILARITY: Contains 1 CARD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Spleen;
TISSUE=Sploin1:2; PubMed=8945639;
Digby M.R., Kimpton W.G., York J.J., Connick T.E., Lowenthal J.W.;
"ITA, a vertebrate homologue of IAP that is expressed in T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               438 WIQSKREAIVSOMTEACLNQSLDALLSRDLIMKEDYELISTKPTRTSKVRQL 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 FIDQHRAALIARVTN--VEWLLDALYGK-VLTDEQYQAVRAEPTNPSKWRKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.9%; Score 67.5; DB 1; Length 539; 30.8%; Pred. No. 2.9; tive 15; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                           PROSITE; PS50209; CARD; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00108; PROTEIN KINASE ATP; FALSE NEG.
Transferase; Serine-threomine-protein kinase; ATP-binding; Phosphorylation; Apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
42951BF97CA15DFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            CARD.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN KINASE.
                                                                                                                                                                                            MGD, MGI:1891456; Ripk2.
InterPro: IPR0001315; CARD.
InterPro: IPR0001315; CARD.
InterPro: IPR0001245; Tyr_Dkinase.
Pfam; PF00619; CARD; 1.
Pfam; PF00669; pkinase; 1.
PfAMTS: RR00109; TYRINASE.
ProDom; PR000001; Prot kinase; 1.
SWART; SW00114; CARD; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lymphocytes.";
DNA_Cell Biol. 15:981-988(1996)
                                                                                                                                                                                    EMBL; AF461040; AAL96436.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                         60400 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity surverse 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              146
                                                                                                                                                                                                                                                                                                                                                                                                                              146 1
539 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus.
NCBI_TaxID=9031;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                              13
STRAIN=White leghorn, TISSUE-Embryonic fibroblast;
MEDLINE-98038801; PubMed-9372964;
MEDLINE-98038801; PubMed-9372964;
N. P.-T., Hrdlickova R., Boe H.R. Jr.;
"ch.IAP1, a member of the inhibitor-of-apoptosis protein family, is mediator of the antiapoptotic activity of the v-Rel oncoprotein.";
mediator of the antiapoptotic activity of the v-Rel oncoprotein.";
mediator of the state of the state of the v-Rel oncoprotein.";
-1- FUNCTION: Apoptobic suppressor.
-1- SUBCELLULAR LOCATION: Predominantly nuclear. Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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17.6%; Score 66.5; DB 1; Length 611;
Best Local Similarity 32.7%; Pred. No. 4.4;
Matches 17; Conservative 14; Mismatches 20; Indels
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53FC9136F34EBDDD CRC64;
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C -> H (IN REF. 2).
C -> H (IN REF. 2).
C -> F (IN REF. 2).
C -> F (IN REF. 2).
C -> F (IN REF. 2).
C -> F (IN REF. 2).
V -> F (IN REF. 2).
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V -> Y (IN REF. 2).
V -> Y (IN REF. 2).
V -> GQ (IN REF. 2).
V -> GQ (IN REF. 2).
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V -> GQ (IN REF. 2).
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RING-TYPE.
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611 AA;
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Birney E., Hayashizaki Y.;

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MEDINE-228825; PubMed=12477932;

MEDINE-228825; PubMed=12477932;

MILLNE-228825; MILLNE-228826; MILLNE-228826;

MILLNE-228826; MILLNE-228826; MILLNE-228826;

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SEQUENCE OF 1-579 FROM N.A.

SEQUENCE OF 1-579 FROM N.A.

STRAIN=C57BL/6J; TISSUB=Retina;

MEDININ=25354683; DubMed=12466851;

AN MEDININ=25354683; DubMed=12466851;

AN MARIAN TOMARY Y. HARSHKAM T., Adachi J., Bono H., Kondo S.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

A Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Arangin A., Matsuda H., Batalov S., Beisel K.W.,

Baldarelli R., Asangin T.A., Fletcher C.F., Fortest A., Frazer K.S.,

RA Cassterland T., Gariboldi M., Glssi C., Godaik A., Gough J.,

Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Magashima T., Numata K., Okido T., Peavan W.J., Pertea G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Vasai T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

Sandelin A., Schnikawa T., Ronno H., Nakamura M., Sakazume N., Sato K.,

Shiraki T., Waki K., Kawa J., Airawa K., Arakawa T., Pukuda S.,

Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N.,

Shiraki T., Waki K., Kawa J., Airawa K., Shinagawa T., Pukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

Myazaki A., Yashino M., Waterston R., Lander E.S., Rogers J.,

Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
                                                                                                                                                                                                                DX52_MOUSE STANDARD; PRT; 598 AA.
08K301, 08BM29;
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
DRAD-box protein 52 (EC 3.6.1.-) (Putative ATP-dependent RNA helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                          DDXS2 OR ROK1.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                        LHFIDQHRAALIARVTNVEWLLDALY-GKVLTDEQYQAVRAEPTNPSKMRKL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
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                                                                                                                                                         RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------VTNVEWLL----DA 25
           "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNs.";
Nature 420:563-573 (2002).
-!- SUBCELLULAR LOCATION; Nuclear; nucleolar (By similarity).
-!- SUBLITY: Belongs to the DEAD box helicase family.
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TISSUB-Endothelial cells;

MEDLINES-92240667; PubMed=10224040;

MEDLINES-92240667; PubMed=10224040;

Bertin J., Nir W.-J., Fischer C.M., Tayber O.V., Errada P.R.,

Grant J.R., Keilty J.J., Gosselin M.L., Robison K.E., Wong G.H.W.,

Glucksmann M.A., Distefano P.S.;

"Human CARD4 protein is a novel CED-4/Apaf-1 cell death family member.

that activates NF-kappab.";

J. Biol. Chem. 274:12955-12958 (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEAD, ATP HELICASE; FALSE NEG.

Se; Nuclear protein; RNA-binding; ATP-binding.

ATP (BY SIMILARITY).

32 ATP HELICASE; FALSE NEG.

92 POLY-LYS.

75 E -> Q (IN REF. 2).

81 R -> K (IN REF. 2).

103 L -> F (IN REF. 2).

119 E -> D (IN REF. 2).

312 S -> N (IN REF. 2).

312 S -> N (IN REF. 2).

313 I -> V (IN REF. 2).

4 G7442 MW; 07D825A9FICFB8DB CRC64;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 65; DB 1; Length 598;
; Pred. No. 6.4;
14; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |: || || :: || || 324 LFEDGKTGFREQLASIFLACTSPKVRRAMFSATFAYDVEQW-CK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 LY--GKVLTDEQYQAVRAEPTNPSKMRKLFSFTPAWN---WTCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAR4 HUMAN STANDARD; PRT; 953 AA.
09Y239; QBIWF5;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Caspase recruitment domain protein 4 (Nod1 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LHFIDQHRAALIAR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGT:1925644; DGX52.
InterPro; IPR001410; DEAD.
Fid; PF00270; DEAD.
Ffam; PF00270; DEAD; 1.
Ffam; PF00271; DEAD; 1.
Ffam; PF00487; DEXD; 1.
FRART; SM0487; DEXDc; 1.
FROSITE; PS00039; DEAD_ATP_HELICASE Hydrolase; Helicase; Nuclear proced by the bind proced by the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size of the bind size o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27; Conservative
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92
75
75
1103
312
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                                                                                                                                                                                                                                                                                             Strausberg R.L., Felmodel 127,732.

Richards E. S., Grouse L.H., Derge J.G.,

Richards R.L., Felmodel 127,732.

Richards R.L., Felmodel 127, Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodriques S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

Rohnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Rohnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Ruman and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE=21264704; PubMed=11058605; Inchara N., Ogura Y., Chen F.F., Muto A., Nunez G.; Inchara N., Ogura Y., Chen F.F., Muto A., Nunez G.; Inchara N., Ogura Y., Chen F.F., Muto A., Nunez G.; Inchara Seponsiveness to bacterial lipopolysaccharides."; J. Biol. Chem. 276:2554(2001).

-!- FUNCTION: Enhances capase-9-mediated apoptosis. Induces NF-kappa-B activity via RICK (CARDIAK, RIP2) and IKK-gamma. Confers reponsiveness to intracellular bacterial lipopolysaccharides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: Self-associates. Binds to caspase-9 and RICK by CARD-CARD
                                                                                       я.
                                                                             Inohara N., Koseki T., del Peso L., Hu Y., Yee C., Chen S., Carrio J Merino J., Liu D., Ni J., Nunez G.; Nodi, an Apaf-1-like activator of caspase-9 and nuclear factor-kappab...; U. Biol. Chem. 274:14560-14567(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interaction.
--- SUBCELLULAR LOCATION: Cytoplasmic.
--- TISSUE SPECIFICITY: Highly expressed in adult heart, skeletal muscle, pancreas, spleen and ovary. Also detected in placenta, lung, liver, kidney, thymus, testis, small intestine and colon.
--- SIMILARITY: Contains 1 CARD domain.
--- SIMILARITY: Contains 1 NACHT domain.
--- SIMILARITY: Contains 9 leucine-rich (IRR) repeats.
               SEQUENCE FROM N.A., AND MUTAGENESIS OF VAL-41 AND LYS-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; bubsdu; .

MIM; bubsdu; .

MIM; bubsdu; F:caspase activator activity; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0066915; P:apoptosis; TAS.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR001315; CARD.
InterPro; IPR007031; LAR RNinh.
InterPro; IPR007111; NACHT_NTPase.
                                                                 MEDLINE=99262599; PubMed=10329646;
                                                                                                                                                                                                                                                             TISSUE=Lymph;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF126484; AAD29125.1; -. EMBL; AF149774; AAD43922.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AF113925, AAD28350.1; -. EMBL, BC040339, AAH40339.1; -. Genew, HGNC116390; CARD4.
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                          ..
(7
                                                                                                                                                                                                                                                                        41 V-SO: ABOLISHES CASPASE-9 ACTIVATION AND INTERACTION WITH RICK.

K-SR: REDUCES CASPASE-9 ACTIVATION.

K -> H (IN REF. 3).

107690 MW; 0A9DFSFC6487E21A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LHFIDQHRAALIARVTNVEWLLDALYGKVLTDEQYQAVRAE----PTNPSKMRKL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 IQLIKSNRELLVTHIRNTQCLVDNL----LKNDYFSAEDABIVCACPTQPDKVRKI 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=A1,

BUDLINE=29431471; PubMed=9286976;

Swift S., Karlyshev A.V., Fish L., Durant E.L., Winson M.K.,

Chhabra S.R., Williams P., Macintyre S., Stewart G.S.A.B.;

Chhabra S.R., Williams P., Macintyre S., Stewart G.S.A.B.;

Chotoum sensing in Aeromonas hydrophila and Aeromonas salmonicida:

identification of the LuxR1 homologs ApyR1 and AsaR1 and their

cognate N-acylhomoserine lactone signal molecules.";

Bacteriol. 19:5271-5281(1997).

-1. SUBCELLULAR LOCATION: Integral membrane protein (Probable).

-1. SIMILARITY: BELONGS TO THE LYSE/XGGA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                            .
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01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical 24.5 kba protein in ahyR-cdpD intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Proteobacteria, Gammaproteobacteria, Aeromonadales,
Aeromonadaceae, Aeromonas.
                                                                                                                                                                                                                                                                                                                                                                        17.1%; Score 64.5; DB 1; Length 953; 28.6%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                          12; Mismatches 19; Indels
Pfam; PF00619; CARD; 1.
PROSITE; PS50209; NACHT; 1.
PROSITE; PS50209; NACHT; 1.
PROSITE; PS5037; NACHT; 1.
Apoptosis; ATP-binding; Repeat; Leucine-rich repeat.
DOMAIN 196 531 NACHT.
NP BIND 202 209 ATP (POTENTIAL).
REPEAT 702 725 LRR 1.
REPEAT 755 LRR 3.
REPEAT 755 LRR 3.
REPEAT 755 LRR 5.
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InterPro; IPRUOLLS:
Pfam; PF01810; LySE; 1.
TIGRFAMS; TIGR00948; 2a75; 1.
Hypothetical protein; Transmembrane.
Thysoken 1 21 POTENTIAL
Thysoken 2 57 POTENTIAL
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                                                                                                                                               LERR 2.
LERR 4.
LERR 5.
LERR 6.
LERR 7.
LERR 8.
LERR 9.
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Interpro; IPR001123; LysE.
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Best Local Similarity 28.6%
Matches 16; Conservative
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447 4
953 AA;
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CONFLICT
SEQUENCE
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MUTAGEN
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REPEAT
REPEAT
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YGGA_AERHY
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SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.
SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.
INDARA N., del Peso L., Koseki T., Chen S., Nunez G.;
INDARA N., del Peso L., Koseki T., Chen S., Nunez G.;
"RICK, a novel protein kinase containing a caspase recruitment domain, interacts with CLARP and regulates CD95-mediated apoptosis.";
                                                                                                  1 GLHFIDQHRAAL--IARVTNVEWLLDALYGKVLTDEQYQAVRAEPTNPSKMRKLFSFTPA
                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
11-0CT-2003 (Rel. 42, Last annotation update)
(RIP-1ike interacting CLARP kinase) (Receptor-interacting protein 2)
(RIP-1ike interacting CLARP kinase) (Receptor-interacting protein 2)
(RIP-2) (CARD-containing interleukin-1 beta converting enzyme associated kinase) (CARD-containing IL-1 beta ICE-kinase).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Skin;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND MUTAGENESIS OF ASP-146.
MEDLINE=98381580; PubMed=9705938;
MATTIONE M., Hoffmann K., Burns K., Martinon F., Bodmer J.-L.,
Mattmann C., Tschopp J.
"Identification of CARDIAK, a RIP-like kinase that associates with
                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NOBI_TaxID=9606;
                                                                              5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.
TISSUB-Endothelial cells;
MEDLINE=98307936; Pubmed=9642260;
MEDLINE=98307936; Dixit V.M.;
"KIP2 is a novel NF-kappaB-activating and cell death-inducing
                                                        DB 1; Length 225;
                                                                            33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Ozersky P., Holmes A., Broy M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ databases
                                172DB104473B0B09 CRC64;
                                                      ch 16.5%; Score 62.5; DB Similarity 24.6%; Pred. No. 4.3; 16; Conservative 11; Mismatches
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 273:16968-16975(1998)
65 85 POT
116 136 POT
150 170 POT
225 AA; 24482 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Curr. Biol. 8:885-888(1998).
[4]
                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Platzer M., Varon R.,
Submitted (DEC-1998) t
                                                                                                                                                                    194 WGWRC 198
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                                                                                                                                              WNWTC 63
                                                                                                                                                                                                                          RIK2 HUMAN
043353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kinase.";
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TRANSMEM
TRANSMEM
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SEQUENCE
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Best Local S
Matches 16
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Procession M.J. Useful T. B., Paters A. Rehalo M. Hoog B. Brownstein M.J. Useful T. B., Toshiyali S., Cannuld P. P. Brows S. S., Loquellano N.J. Watern D. J. A. Character T. B. Brownstein M.J. Useful T. B., Toshiyali S., Cannuld P. M. Garden P. J., Mallady S. J., Black S. M. Kodenn P. J., McKernan N.J. Maled M. A. Gardiner B. H., Michael D. J. J. Mallady A. M. Garden P. J., Mallady J. Black S. M. Kodenn P. J. M. Kokrann N.J. Amide M. A. Gardiner B. H., Michael S. W. Morley P. M. J. Mallady J. Black S. M. Modenn P. J. M. Mallady J. Black S. M. Madan J. Followship M. Madan J. Followship M. Madan J. Followship M. Madan J. Followship M. Madan J. W. Garden M. J. Mallade B. J. Mallade M. M. Madan J. Mallade M. M. Madan J. M. Malladan J. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mallade M. Mal
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Job time : 7.84337 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
DEAD-box protein 52 (EC 3.6.1.-) (Putative ATP-dependent RNA helicase DEXST-like) (FROKIL).
                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Mismatches 19; Indels 44; Gaps
                                                                                                                                                                                                                                                 4 FIDQHRAALIARVTN--VEWILLDALYGK-VLTDEQYQAVRAEPTNPSKMRKLFSFT 56
K->M: REDUCES FAS-MEDIATED APOPTOSIS.
D->N: ABOLISHES KINASE ACTIVITY.
575A692239505792 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB055628; BAB32441.1; -.

HSSP; Q58083; 1HV8.

InterPro; IPR001410; DEAD.

Ffam; PF00270; DEAD; 1.

Pfam; PF00271; helicase C; 1.

SMART; SM00497; DEAD; 1.

PROSITE; PS00039; DEAD ATP HELICASE; FALSE NEG.

Hydrolses; Helicase; Nuclear protein; RNA-binding.

NP BIND 210 217 ATP DEAD BAD ATP DEAD BOX.

SITE 319 322 DEAD BOX.
                                                                                                                                                                                          <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIW, Suzuki T.;
"Identification of a novel ROK1-like protein in rat brain.";
"Identification of to the EMBL/GenBank/DDBJ databases.
Submitted (FBB-2011) to the EMBL/GenBank/DDBJ databases.
-: SUBCELULAR LOCATION: Nuclear; nucleolar (By similarity).
-: SIMILARITY: Belongs to the DEAD box helicase family.
                                                                                                                        Query Match 16.5%; Score 62.5; DB 1; Length 540; Best Local Similarity 30.4%; Pred. No. 11; Matches 17; Conservative 13; Mismatches 23; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.4%; Score 62; DB 1; Length 598; 25.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |: || :| || || 324 LFEDGKTGFRDQLASIFLACTSPKVRRAMFSATFAYDVEQW-CK 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-LYS.
; B9E818EA6B144425 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         598 AA.
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67239 MW;
                                                                    61194 MW;
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Best Local Similarity 25.04
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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      47
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146 1
540 AA;
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598 AA;
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   MUTAGEN
MUTAGEN
SEQUENCE
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099PT0;
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                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
DX52_RAT
DX52_RAT
DY52_RAT
DY52_RAT
DY50_DT 10-0C
DT 10-0C
DT 10-0C
DT 10-0C
DT 10-0C
DT 10-0C
DE REALT
CO Mamma
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RESULT 1 Q8HXK9

ALIGNMENTS

09XDX6 093R39 0921C9

Q9RHG7

SEQUENCE FROM N.A.
Masumoto J., Zhou W., Chen F.F., Su F., Kuwada J.Y., Hidaka E.,
Katsuyama T., Sagara J., Taniguchi S., Ngo-Hazelett P.,
Postlethwalt J.H., Nunez G., Inohara N.;
Caspy: A Zebrafish caspase activated by ASC oligomerization required
for pharyngeal Arch development."; Bos taurus (Bovine). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos. 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Apoptosis-associated speck-like protein containing a CARD. BASC. 195 AA PRT; PRELIMINARY; Q8HXK9

Q8hxk9 bos taurus

Description

B

Query Match Length

Score

Result No.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_rvirus:*
sp_bacteriap:*

archeap:*

SUMMARIES

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINES-20365608, PubMed=10567338;

Masumcto J., Taniguchi S., Ayukawa K., Sarvotham H., Kishino T.,

Niikawa N., Hidaka E., Katsuyama T., Higuchi T., Sagara J.;

Niikawa N., Hidaka E., Extsuyama T., Higuchi T., Sagara J.;

Niikawa N., Hidaka E., Fatsuyama T., Higuchi T., Sagara J.;

Novel 2-Kba protein, aggregates during apoptosis of human promyelocytic leukemia Hi-60 cells.";

J. Biol. Chem. 274:33835-33838(1999).

Q8chk8 rattus norv Q8chs9 mus musculu Q8chs3 mus musculu Q8chs1 mycobacteri Q9chl2 mycobacteri Q9chs9 chimpanzee Q8chs7 chimpanzee Q8chs7 chimpanzee Q8chs7 chimpanzee Q8chs7 chimpanzee Q8chy9 corynabacte Q8fty0 corynabacte Q8fty0 corynabacte Q8chs2 ictalurus p Q8chs2 ictalurus p Q8chs2 ictalurus p Q8chs2 ictalurus p Q8chs2 ictalurus p Q8chs2 ictalurus p Q8chs2 ictalurus p Q8chs2 ictalurus p Q8chs2 ictalurus p Q8chs2 ictalurus p

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303 269 73.5 69.5 68 67 67 67

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Q8FTY0 Q804E2 Q8UWD2 Q7T0K2

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MEDLINE-20580347; PubMed=11139337;
MEDLINE-20580347; PubMed=11139337;
Masumoto J., Taniguchi S., Nakayama K., Ayukawa K., Sagara J.;
Muxine ortholog of ASC, a CARD-containing protein, self-associates, and exhibits restricted distribution in developing mouse embryos.";
EXP. Cell Res. 262.128-133(2001).
EXBL; ABOSO006; BAC43753.1; GO, GO:0005622; C:intracellular; IEA.

arabidopsis arabidopsis campylobact

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12 IDRERKRIVETIQADSGLLLDALVARGVLTGPEYEALDALPDAERRMRRLLLLIVQSKGEA 71
                                                                                                                                                                                                                                                               The FANTOM Consortium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
whals of the mouse transcriptome based on functional annotation of
60,770 full-length oDNAs.;
Nature 420:563-573 (2002).
Nature 420:563-573 (2002).
GO, GO:0005622; C:intracellular; IEA.
GO, GO:0016329; F:apoptosis regulator activity; IEA.
GO, GO:0006915; P:apoptosis regulator activity; IEA.
InterPro; IPR001315; CARD.
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Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Strausberg R.;
Strausberg R.;
Submitteed (AFR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC027290, AAH27290.1; -
RGD; MGI:1925938; B430311C09Rik.
R GO; GO:0005622; C:intracellular; IEA.
R GO; GO:0005622; F:apoptcsis regulator activity; IEA.
R GO; GO:0006329; F:apoptcsis, IEA.
R InterPro; IPR001315; CARD.
SMART; SM00114; CARD.
SMART; SM00114; CARD.
SRQUENCE 220 AA; 24627 MW; A4DCD5606EB320A2 CRC64;
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PROSITE; PS50209; CARD; 1.
SEQUENCE 220 AA; 24599 MW; B8B16AC2EC3071F2 CRC64;
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Apoptosis repressor with CARD domain.
B430311C09RIK.
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STRAIN=C57BL/6J; TISSUE=Hypothalamus;
MEDLINE=22354683; PubMed=12466851;
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Matches 22; Conservative
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Katsuyama T., Sagara J., Taniguchi S., Ngo-Hazelett P.,
Postlethwait J.H., Nunez G., Inohara N.;
Caspy: A Zebrafic aspase activated by ASC oligomerization required
for pharyngeal Arch development.";
J. Biol. Chem. 0:0-0(2002).
EMBL; AB053165; BAC43754-11;
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0016329; F:apoptosis regulator activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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INTERPRO; IPR004020; PAAD_DAPIN_dom.
Pfam; PF02758; PAAD_DAPIN; 1.
PROSITE; PS52029; CARD; 1.
SEQUENCE 193 AA; 21654 MW; F3B27B560D86A17B CRC64;
GO, GO:0016329; F:apoptosis regulator activity; IEA. GO; GO:0006915; P:apoptosis; IEA. InterPro; IPR00401315; CARD. InterPro; IPR004020; PAAD DAPIN dom. PF02758; PAAD DAPIN 1. PROSTIE; PS05029; CARD, 1. PROSTIE; PS05029; DAPIN; 1. SEQUENCE 195 AA; 21917 MW; 7C9D4BDBDBA9A9E8 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UJW-2003 (TrEMBLrel. 24, Last annotation update)
Apoptosis-associated speck-like protein.
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Matches 52; Conservative
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Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
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SEQUENCE FROM N.A.

MEDLINE-2480.29 bubMed=1256656;

Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,

Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,

Fleirs M.W.B.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,

Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing

De Vos W.M., Siezen R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OTN-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter ATP-binding protein, possibly in EF-3 subfamily.
ML1816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete genome sequence of Lactobacillus plantarum WCFS1.";
Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995 (2003).

BMBL, AL935257, Cab64145.1; -

GO; GO:0006483; F:transaminase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

InterPro; IPR005814; Aminotrans. 3.

Pfam, PF00202; aminotrans. 3.

Pfam, PF00202; aminotrans. 4.9 Aminotransferase; Complete proteome.

SEQUENCE 449 AA, 49491 MW; E2CD4FEF25F69E0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corymebacterinees, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1769,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.0%; Score 68; DB 16; Length 449; 27.2%; Pred. No. 7.7; tive 13; Mismatches 22; Indels 2
                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Aminotransferase (EC 2.6.1.-).
                                                                                                                                                                                   449 AA.
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                                                                                                                                                                                   PRT;
                        61
                                                                 72 ACQELLRCAQQTVRMPDPAWDW 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 PRVVKAIQEQAAKLIHYTPAY 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 27.2
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                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                            Lactobacillus plantarum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1590;
                        57
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                                                                                                                                                                                 Q88WC4
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Matches
                                                                                                                                          RESULT 5
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Waltani R., Ota T., Storbatake N., Inagaki H., Ikema Y., Okamoto S., Rawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., A. Kitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., A. Atanaka T., Isogai T., Sugano S.; A. Atanaka T., Isogai T., Sugano S.; Ribahara T., Ramama D., Ramama D., Solollo Che E., Ballisa C., Colollo Che E., Ballisa C., Colollo Che E., Ballisa C., Cartacellular, IEA.

B. Gololos Sololos G., Cartacellular, IEA.

B. Gololos Sololos S., RabGap T., Cartacellular, IEA.

B. Gololos Sololos S., RabGap T., Cartacellular, IEA.

B. Ramar, Proofed, TBC, 1.

B. Ramar, Shoolos S., Sanatotropin.

B. Ramar, Shoolos S., Somatotropin.

B. Ramar, Shoolos S., Somatotropin.

B. Rosolis, Solos Somatotropin.

B. Rosolis, Solos Somatotropin.

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B. Rosolis, Solos Somatotropin.
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د.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 HNVELIAAVVNRVWFLDAVLGKVDVYNMGWYKYLDSRATDEQRR--RRERVNAER 278
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 HRAALIARVINVEWLLDALYGKV------LIDEQYQAVRAEPINPSK 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GLHFIDQHRAALIARVTNVE----WLLDALYGKVLTDEQYQAVRAEPTNPSKWRKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                         Leprona, M11816; ---

GO; GO: 0015620; C: membrane; IEA.

GO; GO: 0005524; F: ATP binding; IEA.

GO; GO: 000509; F: ATP-binding cassette (ABC) transporter acti...

GO; GO: 0006166; F: mucleotide binding; IEA.

GO; GO: 0006810; P: transport; IEA.

InterPro; IPR00359; AAA, ArPase.

InterPro; IPR003439; ABC_transporter.

PEdm; PE00006; ABC transporter; 2.

SMART; SM00382; AAA; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.0%; Score 68; DB 16; Length 545; 36.4%; Pred. No. 9.7; tive 3; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.7%; Score 67; DB 4; Length 257; 33.9%; Pred. No. 5.2; tive 10; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              il protein. -
257 AA; 28960 MW; 5B0A7E5779DF2B94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
ATP-binding; Complete proteome.
SEQUENCE 545 AA; 58986 MW; 75AAA463EB91FBCD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein FLJ22474.
                                                                                                                                    "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EMBL, ALS83923; CAC30769.1; -.
PIR, A87136; A87136.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 36.4 nes 20; Conservative
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flesh-eater.";
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Q882B7
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S Y R R R R R R R R S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hirsch V.M., Campbell B.J., Bailes E., Goeken R., Brown C., Elkins W.R., Axthelm M., Murphey-Corb M., Sharp P.M.; Characterization of a novel simian immunodeficiency virus (SIV) from L'Hoest monkeys (Cercopithecus l'hoesti): implications for the origins of SIVmnd and other primate lentiviruses."; Jurol. 73:1036-1045(1999).
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STRAIN=13 / Type A;
MEDLINE=21664373; PubMed=11792842;
Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coat protein; Glycoprotein; Polyprotein; Transmembrane.
ICE 912 AA; 104904 MW; 70FE8E016922DAAC CRC64;
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                                                                                                                                                                                                                                                                                                                                                         Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV). Viruses; Retroid viruses; Retroviridae; Lentivirus. NCBI_TaxID=11723;
                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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29.0%; Pred. No. 24;
ive 7; Mismatches 19;
                                                                                                             912 AA
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                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=SIVlhoest;
MEDLINE=99098990; PubMed=9882304;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 TNVEWLLD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=SIV1hoest;
                                                                                                                                                                                                                                                                                                      Envelope protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|
SW 702
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                                                                                                             090278
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                                   RESULT 8
090278
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Q8XNW6
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                                                                   transporter acti. . .; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D., Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M., Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S., Bennan M., Haft D., Selngut J., Nelson W., Davidsen T., White O., Fraser C., Collmer A.; Slengut J., Nelson W., Davidsen T., "Complete sequence of Pseudomonas syringae."; Submitted (MAR.2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                   ö
                                                                                                                                                                               Score 67; DB 16; Length 1175;
Pred. No. 33;
8; Mismatches 22; Indels
                                                                                                                                                                                                                                                                    924 IEEYDNNLIKIKANIELLIKKLNGKSLTEEEWTRVLQEKNNTEKELK 970
Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

EMBL, APRO3185; BAB79922.1, .

GO, GO:0016629; E:MPT binding; IEA.

GO, GO:0004609; F:ATP binding cassette (ABC) transporter

GO; GO:0004612; F:ATP-binding cassette (ABC) transporter

GO; GO:0004617; F:exonucless activity; IEA.

GO; GO:0004817; F:exonucless activity; IEA.

GO; GO:0004817; F:exonucless activity; IEA.

Exonucless; Complete protecome

Exonucless; Complete protecome

Exonucless; Complete protecome

Exonucless; Complete protecome

Exonucless; Complete protecome

Exonucless; ABC Transporter.
                                                                                                                                                                                                                                                 5 IDQHRAALIARVTNVEWLLDALYGKVLTDEQYQAVRAEPTNPSKMRK
                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-QCT-2003 (TrEMBLrel. 25, Last annotation update)
Sensor histidine kinase/response regulator.
                                                                                                                                                                                                                                                                                                                                                                 PRT; 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carrier
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas syringae (pv. tomato).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003018; GAF.
InterPro; IPR005467; His kinase.
InterPro; IPR003661; His kina N.
InterPro; IPR003006; Ig MrC.
InterPro; IPR001993; Mitoch carrie
InterPro; IPR001789; Response_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF05227; CHASE3; 1.
Pfam; PF01590; GAF; 1.
Pfam; PF01590; GAF; 1.
Pfam; PF00512; HisKa; 1.
Pfam; PF00721; HisKa; 1.
PRINTS; PR00721; response reg; 3.
PRINTS; PR00344; BCTRLSENSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonadaceae; Pseudomonas
                                                                                                                                                                                Query Match
Best Local Similarity 36.2%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Length 149;

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SEQUENCE FROM N. A.

PEQUENER FROM N. A.

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"Cloning of anti-apoptotic genes in non-specific cytotoxic cells.";

Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

BERL; AY184377; AA024632.1;

CO; GO:0008189; Fiapoptosis inhibitor activity; IEA.

GO; GO:0008189; Fiapoptosis inhibitor activity; IEA.

RO; GO:0008189; Fiapoptosis inhibitor activity; IEA.

RO; GO:0008189; Fiapoptosis; IEA.

RITE-PRO; IPR001315; CARD.

RITE-PRO; IPR001315; CARD.

RITE-PRO; IPR001315; CARD.

RITE-PRO; IPR001315; CARD.

REAM; PR00653; BIR, 3.

RART; SM00114; CARD; 1.

RART; SM00114; CARD; 1.

RART; SM00118; RING; 1.

ROSITE; PS501282; BIR, REPEAT_1; 2.

ROSITE; PS50089; CARD; 1.

ROSITE; PS50089; CARD; 1.

RECOILE: PS50089; CARD; 1.

RECOILE: PS50089; CARD; 1.
STRAIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y., Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y., Usuda Y., Sugimoto S.; Ruthe entire genomic sequence of Corynebacterium efficiens YS-314.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP065214; BAC17053.1; --
Hypothetical protein; Complete proteome.
SEQUENCE 149 AA; 16334 MW; D11861ADB491A4F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ictalurus punctatus (Channel catfish).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Siluriformes,
Ictaluridae, Ictalurus.
NCBI_TaxID=7998;
                                                                                                                                                                                                                                                                                                                                                                                                                                7 OHRAALIARVINVE--WLLDALYGKVLTDEQYQAVRAEPINPSKMRKLFSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   455 GFTFLKKHHAALTQRLKSVQSLMDHLLEENVISQKEYDTIR 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                   DB 16;
                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                Query Match
17.3%; Score 65.5; DE
Best Local Similarity 32.7%; Pred. No. 4.1;
Matches 17; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ą
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Local Similarity 34.1%; Pred. No. 23;
les 14; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibitor of apoptosis protein-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
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01-MAR-2002
01-MAR-2002
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003
01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q804E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q804E2
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Matches
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Q804E2
ID Q804E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8UWD2
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                 SERRERES
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                                                                                                                                                                                                                                                                                                                                                                        82 HFLDPYEIAKPLLVAELNGLQD------LUKDNPTQQDRFRRLFTMQQEWNVF 128
                                                                                                                                                                                                                                                                                                                   3 HFIDQHRAALIARVTNVEWLLDALYGKVLTDEQYQAVRAEPTNPSKMRKLFSFTPAWNWT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GLHFIDQHRAALIARVTNVB----WLLDALYGKVLTDEQYQAVRAEPTNPSKMRKL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8N528 PRELIMINARY; PRT; 249 AA.
Q8N528;
Q8N528;
Q1-OCT-2002 (TrEMBLrel. 22, Created)
O1-OCT-2002 (TrEMBLrel. 24, Last sequence update)
O1-TON-2003 (TrEMBLrel. 24, Last annotation update)
Similar to hypothetical protein FLJ22474.
Homo sappiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                          Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterium efficiens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Indels
           PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS00290; IG_MHC; 1.
PROSITE; PS00210; MITOCH CARRIER; 1.
PROSITE; PS50110; RESPONSE_REGULATORY; 3.
Kinase; Complete proteome.
SEQUENCE 1170 AA; 131102 MW; RC649FC4DC65B05B CRC64;
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28446 MW; 49B1F860770F5438 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                            26;
                                                                                                                                                                                                          DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 17.5%; Score 66; DB 4;
Best Local Similarity 33.9%; Pred. No. 6.7;
Matches 19; Conservative 10; Mismatches 15
                                                                                                                                                                                                    Query Match
17.6%; Score 66.5; DB
Best Local Similarity 24.6%; Pred. No. 38;
Matches 16; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE, PS00338; SOMATOTROPIN_2; 1.
PROSITE; PS50086; TBC_RABGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 23, CTrEMBLrel. 23, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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SEQUENCE 249 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Pancreas;
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01-MAR-2003
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SEQUENCE B
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                       Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii; Teleostei; Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
NCBI_TaxID=7955;
                                                                                                       SEQUENCE FROM N.A. MEDINE=20373792; PubMed=10917738; Inohara N., Nunez G.; Inohara N., Nunez G.; "Genes with homology to mammalian apoptosis regulators identified in zebrafish.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13; Length 628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ens K.M., Valdimarsson G.;
"Zebzafish inhibitor of apoptosis protein.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY247786; AAP04483.1;
SEQUENCE 647 AA; 72183 WW; 88DBBAFE92718FA9 CRC64;
                                                                                                                                                                                                       SEQUENCE FROM N.A.
Inohaza N., Nunez G.;
Submitted (1007-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                          EMBL; AF442500; AAL33679.1; --
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0006199; F:apri-apoptosis inhibitor activity; IEA.
GO; GO:0006199; F:atri-apoptosis; IEA.
InterPro; IPR001370; BIR,
InterPro; IPR001315; CARD.
InterPro; IPR001841; Znf ring.
Pfam; PF00659; BIR; 3.
Pfam; PF00699; Zf-C3HC4; 1.
Pfam; PF00097; Zf-C3HC4; 1.
SMART; SM00114; CARD; 1.
SMART; SM00114; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01262, BIR REPEAT 1; 2.
PROSITE; PS50143; BIR_REPEAT_2; 3.
PROSITE; PS50209; CARD; 1.
PROSITE; PS50089; ZR ING 2; 1.
Metal-binding; Zinc; Zinc-finger.
SEQUENCE 628 AA; 70098 MW; 5B68CEB6A87C8A95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 GFTFLKGHAALSQRLKSVQSLMDHLLEENVISQKEYDSIR 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GLHFIDOHRAALIARVINVEWLLDALYGK-VLTDEOYQAVR 40
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                                                                                                                                                                            Cell Death Differ. 7:509-510(2000).
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nes 14; Conserv
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Matches
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